



## SEQUENCE LISTING

<110> Egan, Sean E.  
Wang, Wei  
Sengar, Ameet

<120> ESE GENES AND PROTEINS

<130> 3477.89

<140> US 09/674,237

<141> 1999-04-27

<150> PCT/CA99/00375

<151> 1999-04-27

<150> US 60/118,739

<151> 1999-02-05

<150> CA 2230201

<151> 1998-04-27

<160> 35

<170> PatentIn version 3.2

<210> 1

<211> 5084

<212> DNA

<213> Mus musculus

<400> 1

cggcacgagg	aggagtggag	cggcgcgggg	gggcgcgcag	cttggttgct	ccgtagtacg	60
gcggctcgca	agggagcatc	ccgagcgggc	tccgggacgg	ccgggaggca	ggcaggcggg	120
cgggcgggga	tgggtgtgcg	ggctgcggac	tcggcgttcc	tcgcgcggcg	tgcgggctgc	180
actgatttgt	gtgaggggcg	gccgcgcgca	cccgcccgga	gatgaggcgt	cgatcagcaa	240
ggtgaacgta	atagaaccat	ggctcagttt	cccacacctt	tcggtggtag	cctggatgtc	300
tgggccataa	ctgtggagga	aagggccaag	catgaccagc	agttccttag	cctgaagccg	360
atagcgggat	ttattactgg	tgatcaagcg	aggaactttt	ttttccaatc	tgggttacct	420
cagcctgtct	tagcacaaat	atgggcgcta	gcggacatga	ataacgatgg	aaggatggat	480
caagtggaat	tttccatagc	catgaagctt	atcaaactga	agctacaagg	atatcagctc	540
ccctccacac	ttccccctgt	catgaaacag	caaccagtgg	ctatttccag	tgcaccagca	600
tttggtatag	gagggtattg	tagcatgcc	ccactcacag	ctgttgctcc	tgtgccaatg	660
ggctccattc	cagttgttgg	aatgtctcca	cccttagtat	cttctgtccc	tccagcagca	720
gtgcctcccc	tggctaacgg	ggctcctccc	gtcatacagc	ctctgcctgc	gtttgcgcat	780

cctgcagcca	catggccaaa	gagttcttcc	ttcagcagat	ctggtccagg	gtcacaatta	840
aacactaagt	tacagaaggc	acaatcattc	gatgtcgcca	gcgcccctcc	agcagcagaa	900
tgggctgtgc	ctcagtcatc	aaggctgaaa	tacaggcagt	tattcaacag	ccacgacaaa	960
actatgagtg	gacacttaac	aggtccccag	gcaagaacta	ttctcatgca	atcaagttta	1020
ccccaggctc	agctggcttc	aatatggaat	ctttctgaca	ttgatcaaga	tggaaaactc	1080
actgcagaag	aatttatcct	agctatgcac	ctaattgatg	ttgccatgtc	tggtcagcca	1140
ctgccgcccc	tcctgcctcc	agaatacatc	cctccttcct	tcagaagagt	tcgctccggc	1200
agtgggatgt	ccgtcataag	ctcttcttct	gtggatcaga	ggctgcctga	ggagccgtcg	1260
tcagaggatg	agcagcagcc	agagaagaaa	ctgcctgtga	catttgaaga	taagaagcgg	1320
gagaacttcg	agcgaggcag	tgtggagctg	gagaagcgc	gccaaagcgt	cttggagcag	1380
cagcgcaaag	agcaggagcg	gttggctcag	ctggagcgcg	ccgagcagga	gaggaaagag	1440
cgggagcgcc	aggagcagga	ggccaagcgg	cagctggagc	tggagaagca	gctggagaag	1500
cagcgggagc	tggagcggca	gcgagaggag	gagaggagga	aggagatcga	gaggcgcgag	1560
gccgcaaaac	gggaactgga	aaggcagcga	caacttgaat	gggaacggaa	ccggagacag	1620
gaactcctga	atcagaggaa	caaggagcag	gagggcaccg	tggtcctgaa	ggcaaggagg	1680
aagactctgg	agtttgagtt	agaagctctg	aatgacaaaa	agcatcagct	agaaggaaaa	1740
cttcaggata	tcaggtgtcg	actggcaacc	cagaggcaag	aaattgagag	cacgaacaag	1800
tctagagagc	taagaattgc	tgaaatcacc	cacttacagc	agcagttgca	ggaatctcag	1860
caaatgcttg	gaagacttat	tccagagaaa	cagatactca	gtgaccagtt	aaaacaagtc	1920
cagcagaaca	gtttgcatag	agactcgctt	cttaccctca	aaagagcctt	ggaagcaaa	1980
gagctggccc	ggcagcagct	ccgggagcag	ctggacgagg	tggagagaga	gaccaggtca	2040
aagctgcagg	agattgatgt	tttcaacaac	cagctgaagg	aactgagaga	gatacatagc	2100
aaacagcaac	tccagaagca	gaggtccctg	gaggcagcgc	gactgaagca	gaaagagcag	2160
gagaggaaga	gcctggagtt	agagaagcaa	aaggaagacg	ctcagagacg	agttcaggaa	2220
agggacaagc	aatggctgga	gcatgtgcag	caggaggagc	agccacgccc	ccggaaaacc	2280
cacgaggagg	acagactgaa	gaggaagac	agtgtcagga	agaaggaggc	ggaagagaga	2340
gccaaagcgg	aaatgcaaga	caagcagagt	cggcttttcc	atccgcatca	ggagccagct	2400
aagctggcca	cccaggcacc	ctggtctacc	acagagaaa	gcccgcctac	catttctgca	2460

caggagagtg	taaaagtgg	atattaccga	gcgctgtacc	cctttgaatc	cagaagtcac	2520
gatgagatca	ccatccagcc	aggagatata	gtcatgggtg	atgaaagcca	gactggagag	2580
ccaggatggc	ttggaggaga	gctgaaaggg	aagacgggat	ggttccctgc	aaactatgca	2640
gaaaagattc	cagaaaatga	ggttcccact	ccagccaaac	cagtgaccga	tctgacatct	2700
gcccctgccc	ccaaactggc	tctgcgtgag	acccctgctc	ctttgccagt	gacctcttct	2760
gagccctcca	caacccccaa	caactgggca	gacttcagtt	ccacgtggcc	cagcagctca	2820
aacgagaagc	cagaaacgga	caactgggat	acgtggggcg	ctcagccttc	tctgaccgta	2880
cctagtgtctg	gccagttacg	gcagagatca	gcctttaccc	cagccacagc	cactggctcc	2940
tccccatctc	ccgtcctggg	ccaggggtgaa	aaggtggaag	ggctacaagc	gcaagccctg	3000
tatccctgga	gagccaaaaa	agacaaccac	ttaaatttta	acaaaagtga	cgatcatcacc	3060
gttctggaac	agcaagacat	gtgggtggtt	ggagaagttc	aaggtcagaa	gggttggttc	3120
cccaagtctt	acgtgaaact	catttcaggg	cccgtaagga	aatccacaag	catcgatact	3180
ggccctactg	aaagtccctgc	tagtctaaag	agagtggctt	ccccggccgc	caagccagcc	3240
attcccggag	aagagtttat	tgccatgtac	acatacgaga	gttctgagca	aggagattta	3300
acctttcagc	aaggggatgt	gattgtggtt	accaagaaag	atgggtgactg	gtggacggga	3360
acgggtggcg	acaagtcg	agtcttcctt	tctaactatg	tgaggcttaa	agattcagag	3420
ggctctggaa	ctgctgggaa	aacagggagt	ttaggaaaaa	aacctgaaat	tgcccagggtt	3480
attgcttctt	acgtgctac	tggtcccgaa	caactcacc	tggtcctgg	gcagctgatt	3540
ctgatccgga	aaaagaaccc	aggtggatgg	tggaaggag	aactgcaagc	tcgagggaaa	3600
aagcgccaga	taggggtggtt	tccagcaaat	tatgtcaaac	ttctaagccc	cgaacaagc	3660
aaaatcacc	caactgagct	accaagacc	gcagtgcagc	cagcagtgtg	ccaggtgatc	3720
gggatgtacg	attacaccgc	ccagaacgat	gacgaactag	ccttcagcaa	aggccagatc	3780
atcaacgtcc	tcaacaagga	ggaccgac	tggtggaaag	gagaagtcag	tgggcaagtt	3840
gggtcttcc	catccaatta	tgtaaagctg	accacagaca	tggacccag	ccagcaatga	3900
atcatatgtt	gtccatcccc	ccctcaggct	tgaaagtcct	caaagagacc	cactatccca	3960
tatcactgcc	cagagggatg	atgggagatg	cagccttgat	catgtgactt	gcagcatgat	4020
cacctactgc	cttctgagta	gaagaactca	ctgcagagca	gtttacctca	tttgacctta	4080
gttgcatgtg	atcgaaatgt	ctgagtcact	gcgtgcagag	gcagaagcaa	attgcagaac	4140
tgcacaggg	ggtgggtcct	tttggggctt	tcctagtcac	tcagactgac	cggccccgcc	4200

```

ttcacacggg cgctttcaat agttttaaga ttatttttaa atgtgtattt tagcctttta 4260
ataaaaaatct caatcaatta cttctttgccc tatttttggtt ttacaaaaaac acccactatc 4320
aaggagtgccc tgtctgcgga cgattaaaat gctgttccgg gcgtaccgta aactgagagc 4380
ttgctgtacc tttgccgttt gtccagtgtt cccaaccaca ttgtgtagtt tggggctgtt 4440
ccctgccgta gagcacagag gagatgggtg tacctgtttt gaaaatgtgt atgtagactg 4500
agcctgacta tggaaggggt tatgcttgtc tgtgaccatc acgtgtacct gtcgcgcatg 4560
taccatctgt accgaagaag tagctcttcc tccatggcta aaccaccac cgtgtacagt 4620
gctctcatct actgcattca ttttactttg cacagtgacc ttgtagccac ctgaggaagc 4680
acccatgttt ccgtttggtc tcagatgtac ctagtgtgtc ccgtgttttg tttttatttt 4740
tcaatctggc atgtcttcac accataaact agtaagacgc caactgccca ggcggttacg 4800
atcatcagta cccaccgtct tagtctctgt tacgtgaagt ttattccagt tgctttttat 4860
ggaatatctt gaacaagtaa tcttcttgac aagaaagaat gtatagaagt ctccctgcaa 4920
ttaatttccc agtgtttaca ttttttaact agactgtggg ggttgctaca gattaatatg 4980
aaatggcgct cctgggtccgt gtgtgtgtta acttgtgctg tagctgaagc cgtgtgtcct 5040
tagatattag ttggaagtcg ggaagagaat tcgatatcaa gctt 5084

```

```

<210> 2
<211> 3642
<212> DNA
<213> Mus musculus

```

```

<220>
<221> CDS
<222> (1)..(3642)
<223> Mouse Esei

```

```

<400> 2
atg gct cag ttt ccc aca cct ttc ggt ggt agc ctg gat gtc tgg gcc 48
Met Ala Gln Phe Pro Thr Pro Phe Gly Gly Ser Leu Asp Val Trp Ala
1 5 10 15

ata act gtg gag gaa agg gcc aag cat gac cag cag ttc ctt agc ctg 96
Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe Leu Ser Leu
20 25 30

aag ccg ata gcg gga ttt att act ggt gat caa gcg agg aac ttt ttt 144
Lys Pro Ile Ala Gly Phe Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe
35 40 45

ttc caa tct ggg tta cct cag cct gtc tta gca caa ata tgg gcg cta 192

```

Phe	Gln	Ser	Gly	Leu	Pro	Gln	Pro	Val	Leu	Ala	Gln	Ile	Trp	Ala	Leu		
50						55					60						
gcg	gac	atg	aat	aac	gat	gga	agg	atg	gat	caa	gtg	gaa	ttt	tcc	ata		240
Ala	Asp	Met	Asn	Asn	Asp	Gly	Arg	Met	Asp	Gln	Val	Glu	Phe	Ser	Ile		
65					70					75				80			
gcc	atg	aag	ctt	atc	aaa	ctg	aag	cta	caa	gga	tat	cag	ctc	ccc	tcc		288
Ala	Met	Lys	Leu	Ile	Lys	Leu	Lys	Leu	Gln	Gly	Tyr	Gln	Leu	Pro	Ser		
			85					90						95			
aca	ctt	ccc	cct	gtc	atg	aaa	cag	caa	cca	gtg	gct	att	tcc	agt	gca		336
Thr	Leu	Pro	Pro	Val	Met	Lys	Gln	Gln	Pro	Val	Ala	Ile	Ser	Ser	Ala		
			100				105						110				
cca	gca	ttt	ggt	ata	gga	ggg	att	gct	agc	atg	cca	cca	ctc	aca	gct		384
Pro	Ala	Phe	Gly	Ile	Gly	Gly	Ile	Ala	Ser	Met	Pro	Pro	Leu	Thr	Ala		
		115					120						125				
gtt	gct	cct	gtg	cca	atg	ggc	tcc	att	cca	gtt	gtt	gga	atg	tct	cca		432
Val	Ala	Pro	Val	Pro	Met	Gly	Ser	Ile	Pro	Val	Val	Gly	Met	Ser	Pro		
		130				135						140					
ccc	tta	gta	tct	tct	gtc	cct	cca	gca	gca	gtg	cct	ccc	ctg	gct	aac		480
Pro	Leu	Val	Ser	Ser	Val	Pro	Pro	Ala	Ala	Val	Pro	Pro	Leu	Ala	Asn		
145					150					155					160		
ggg	gct	cct	ccc	gtc	ata	cag	cct	ctg	cct	gcg	ttt	gcg	cat	cct	gca		528
Gly	Ala	Pro	Pro	Val	Ile	Gln	Pro	Leu	Pro	Ala	Phe	Ala	His	Pro	Ala		
				165				170						175			
gcc	aca	tgg	cca	aag	agt	tct	tcc	ttc	agc	aga	tct	ggt	cca	ggg	tca		576
Ala	Thr	Trp	Pro	Lys	Ser	Ser	Ser	Phe	Ser	Arg	Ser	Gly	Pro	Gly	Ser		
			180					185					190				
caa	tta	aac	act	aag	tta	cag	aag	gca	caa	tca	ttc	gat	gtc	gcc	agc		624
Gln	Leu	Asn	Thr	Lys	Leu	Gln	Lys	Ala	Gln	Ser	Phe	Asp	Val	Ala	Ser		
		195				200						205					
gcc	cct	cca	gca	gca	gaa	tgg	gct	gtg	cct	cag	tca	tca	agg	ctg	aaa		672
Ala	Pro	Pro	Ala	Ala	Glu	Trp	Ala	Val	Pro	Gln	Ser	Ser	Arg	Leu	Lys		
		210				215					220						
tac	agg	cag	tta	ttc	aac	agc	cac	gac	aaa	act	atg	agt	gga	cac	tta		720
Tyr	Arg	Gln	Leu	Phe	Asn	Ser	His	Asp	Lys	Thr	Met	Ser	Gly	His	Leu		
225					230					235					240		
aca	ggt	ccc	cag	gca	aga	act	att	ctc	atg	caa	tca	agt	tta	ccc	cag		768
Thr	Gly	Pro	Gln	Ala	Arg	Thr	Ile	Leu	Met	Gln	Ser	Ser	Leu	Pro	Gln		
				245				250						255			
gct	cag	ctg	gct	tca	ata	tgg	aat	ctt	tct	gac	att	gat	caa	gat	gga		816
Ala	Gln	Leu	Ala	Ser	Ile	Trp	Asn	Leu	Ser	Asp	Ile	Asp	Gln	Asp	Gly		
			260					265					270				
aaa	ctc	act	gca	gaa	gaa	ttt	atc	cta	gct	atg	cac	cta	att	gat	gtt		864
Lys	Leu	Thr	Ala	Glu	Glu	Phe	Ile	Leu	Ala	Met	His	Leu	Ile	Asp	Val		

275	280	285	
gcc atg tct ggt cag cca ctg ccg ccc gtc ctg cct cca gaa tac atc Ala Met Ser Gly Gln Pro Leu Pro Pro Val Leu Pro Pro Glu Tyr Ile 290 295 300			912
cct cct tcc ttc aga aga gtt cgc tcc ggc agt ggg atg tcc gtc ata Pro Pro Ser Phe Arg Arg Val Arg Ser Gly Ser Gly Met Ser Val Ile 305 310 315 320			960
agc tct tct tct gtg gat cag agg ctg cct gag gag ccg tcg tca gag Ser Ser Ser Ser Val Asp Gln Arg Leu Pro Glu Glu Pro Ser Ser Glu 325 330 335			1008
gat gag cag cag cca gag aag aaa ctg cct gtg aca ttt gaa gat aag Asp Glu Gln Gln Pro Glu Lys Lys Leu Pro Val Thr Phe Glu Asp Lys 340 345 350			1056
aag cgg gag aac ttc gag cga ggc agt gtg gag ctg gag aag cgc cgc Lys Arg Glu Asn Phe Glu Arg Gly Ser Val Glu Leu Glu Lys Arg Arg 355 360 365			1104
caa gcg ctc ttg gag cag cag cgc aaa gag cag gag ccg ttg gct cag Gln Ala Leu Leu Glu Gln Gln Arg Lys Glu Gln Glu Arg Leu Ala Gln 370 375 380			1152
ctg gag cgc gcc gag cag gag agg aaa gag cgg gag cgc cag gag cag Leu Glu Arg Ala Glu Gln Glu Arg Lys Glu Arg Glu Arg Gln Glu Gln 385 390 395 400			1200
gag gcc aag cgg cag ctg gag ctg gag aag cag ctg gag aag cag cgg Glu Ala Lys Arg Gln Leu Glu Leu Glu Lys Gln Leu Glu Lys Gln Arg 405 410 415			1248
gag ctg gag cgg cag cga gag gag gag agg agg aag gag atc gag agg Glu Leu Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg 420 425 430			1296
cgc gag gcc gca aaa cgg gaa ctg gaa agg cag cga caa ctt gaa tgg Arg Glu Ala Ala Lys Arg Glu Leu Glu Arg Gln Arg Gln Leu Glu Trp 435 440 445			1344
gaa cgg aac cgg aga cag gaa ctc ctg aat cag agg aac aag gag cag Glu Arg Asn Arg Arg Gln Glu Leu Leu Asn Gln Arg Asn Lys Glu Gln 450 455 460			1392
gag ggc acc gtg gtc ctg aag gca agg agg aag act ctg gag ttt gag Glu Gly Thr Val Val Leu Lys Ala Arg Arg Lys Thr Leu Glu Phe Glu 465 470 475 480			1440
tta gaa gct ctg aat gac aaa aag cat cag cta gaa gga aaa ctt cag Leu Glu Ala Leu Asn Asp Lys Lys His Gln Leu Glu Gly Lys Leu Gln 485 490 495			1488
gat atc agg tgt cga ctg gca acc cag agg caa gaa att gag agc acg Asp Ile Arg Cys Arg Leu Ala Thr Gln Arg Gln Glu Ile Glu Ser Thr 500 505 510			1536

aac aag tct aga gag cta aga att gct gaa atc acc cac tta cag cag	1584
Asn Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln Gln	
515 520 525	
cag ttg cag gaa tct cag caa atg ctt gga aga ctt att cca gag aaa	1632
Gln Leu Gln Glu Ser Gln Gln Met Leu Gly Arg Leu Ile Pro Glu Lys	
530 535 540	
cag ata ctc agt gac cag tta aaa caa gtc cag cag aac agt ttg cat	1680
Gln Ile Leu Ser Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu His	
545 550 555 560	
aga gac tcg ctt ctt acc ctc aaa aga gcc ttg gaa gca aag gag ctg	1728
Arg Asp Ser Leu Leu Thr Leu Lys Arg Ala Leu Glu Ala Lys Glu Leu	
565 570 575	
gcc cgg cag cag ctc cgg gag cag ctg gac gag gtg gag aga gag acc	1776
Ala Arg Gln Gln Leu Arg Glu Gln Leu Asp Glu Val Glu Arg Glu Thr	
580 585 590	
agg tca aag ctg cag gag att gat gtt ttc aac aac cag ctg aag gaa	1824
Arg Ser Lys Leu Gln Glu Ile Asp Val Phe Asn Asn Gln Leu Lys Glu	
595 600 605	
ctg aga gag ata cat agc aaa cag caa ctc cag aag cag agg tcc ctg	1872
Leu Arg Glu Ile His Ser Lys Gln Gln Leu Gln Lys Gln Arg Ser Leu	
610 615 620	
gag gca gcg cga ctg aag cag aaa gag cag gag agg aag agc ctg gag	1920
Glu Ala Ala Arg Leu Lys Gln Lys Glu Gln Glu Arg Lys Ser Leu Glu	
625 630 635 640	
tta gag aag caa aag gaa gac gct cag aga cga gtt cag gaa agg gac	1968
Leu Glu Lys Gln Lys Glu Asp Ala Gln Arg Arg Val Gln Glu Arg Asp	
645 650 655	
aag caa tgg ctg gag cat gtg cag cag gag gag cag cca cgc ccc cgg	2016
Lys Gln Trp Leu Glu His Val Gln Gln Glu Glu Gln Pro Arg Pro Arg	
660 665 670	
aaa ccc cac gag gag gac aga ctg aag agg gaa gac agt gtc agg aag	2064
Lys Pro His Glu Glu Asp Arg Leu Lys Arg Glu Asp Ser Val Arg Lys	
675 680 685	
aag gag gcg gaa gag aga gcc aag ccg gaa atg caa gac aag cag agt	2112
Lys Glu Ala Glu Glu Arg Ala Lys Pro Glu Met Gln Asp Lys Gln Ser	
690 695 700	
cgg ctt ttc cat ccg cat cag gag cca gct aag ctg gcc acc cag gca	2160
Arg Leu Phe His Pro His Gln Glu Pro Ala Lys Leu Ala Thr Gln Ala	
705 710 715 720	
ccc tgg tct acc aca gag aaa ggc ccg ctt acc att tct gca cag gag	2208
Pro Trp Ser Thr Thr Glu Lys Gly Pro Leu Thr Ile Ser Ala Gln Glu	
725 730 735	

agt gta aaa gtg gta tat tac cga gcg ctg tac ccc ttt gaa tcc aga	2256
Ser Val Lys Val Val Tyr Tyr Arg Ala Leu Tyr Pro Phe Glu Ser Arg	
740 745 750	
agt cac gat gag atc acc atc cag cca gga gat ata gtc atg gtg gat	2304
Ser His Asp Glu Ile Thr Ile Gln Pro Gly Asp Ile Val Met Val Asp	
755 760 765	
gaa agc cag act gga gag cca gga tgg ctt gga gga gag ctg aaa ggg	2352
Glu Ser Gln Thr Gly Glu Pro Gly Trp Leu Gly Gly Glu Leu Lys Gly	
770 775 780	
aag acg gga tgg ttc cct gca aac tat gca gaa aag att cca gaa aat	2400
Lys Thr Gly Trp Phe Pro Ala Asn Tyr Ala Glu Lys Ile Pro Glu Asn	
785 790 795 800	
gag gtt ccc act cca gcc aaa cca gtg acc gat ctg aca tct gcc cct	2448
Glu Val Pro Thr Pro Ala Lys Pro Val Thr Asp Leu Thr Ser Ala Pro	
805 810 815	
gcc ccc aaa ctg gct ctg cgt gag acc cct gct cct ttg cca gtg acc	2496
Ala Pro Lys Leu Ala Leu Arg Glu Thr Pro Ala Pro Leu Pro Val Thr	
820 825 830	
tct tct gag ccc tcc aca acc ccc aac aac tgg gca gac ttc agt tcc	2544
Ser Ser Glu Pro Ser Thr Thr Pro Asn Asn Trp Ala Asp Phe Ser Ser	
835 840 845	
acg tgg ccc agc agc tca aac gag aag cca gaa acg gac aac tgg gat	2592
Thr Trp Pro Ser Ser Ser Asn Glu Lys Pro Glu Thr Asp Asn Trp Asp	
850 855 860	
acg tgg gcg gct cag cct tct ctg acc gta cct agt gct ggc cag tta	2640
Thr Trp Ala Ala Gln Pro Ser Leu Thr Val Pro Ser Ala Gly Gln Leu	
865 870 875 880	
cgg cag aga tca gcc ttt acc cca gcc aca gcc act ggc tcc tcc cca	2688
Arg Gln Arg Ser Ala Phe Thr Pro Ala Thr Ala Thr Gly Ser Ser Pro	
885 890 895	
tct ccc gtc ctg ggc cag ggt gaa aag gtg gaa ggg cta caa gcg caa	2736
Ser Pro Val Leu Gly Gln Gly Glu Lys Val Glu Gly Leu Gln Ala Gln	
900 905 910	
gcc ctg tat ccc tgg aga gcc aaa aaa gac aac cac tta aat ttt aac	2784
Ala Leu Tyr Pro Trp Arg Ala Lys Lys Asp Asn His Leu Asn Phe Asn	
915 920 925	
aaa agt gac gtc atc acc gtt ctg gaa cag caa gac atg tgg tgg ttt	2832
Lys Ser Asp Val Ile Thr Val Leu Glu Gln Gln Asp Met Trp Trp Phe	
930 935 940	
gga gaa gtt caa ggt cag aag ggt tgg ttc ccc aag tct tac gtg aaa	2880
Gly Glu Val Gln Gly Gln Lys Gly Trp Phe Pro Lys Ser Tyr Val Lys	
945 950 955 960	
ctc att tca ggg ccc gta agg aaa tcc aca agc atc gat act ggc cct	2928



Leu Ile Ser Gly Pro Val Arg Lys Ser Thr Ser Ile Asp Thr Gly Pro	
965 970 975	
act gaa agt cct gct agt cta aag aga gtg gct tcc ccg gcc gcc aag	2976
Thr Glu Ser Pro Ala Ser Leu Lys Arg Val Ala Ser Pro Ala Ala Lys	
980 985 990	
cca gcc att ccc gga gaa gag ttt att gcc atg tac aca tac gag agt	3024
Pro Ala Ile Pro Gly Glu Glu Phe Ile Ala Met Tyr Thr Tyr Glu Ser	
995 1000 1005	
tct gag caa gga gat tta acc ttt cag caa ggg gat gtg att gtg	3069
Ser Glu Gln Gly Asp Leu Thr Phe Gln Gln Gly Asp Val Ile Val	
1010 1015 1020	
gtt acc aag aaa gat ggt gac tgg tgg acg gga acg gtg ggc gac	3114
Val Thr Lys Lys Asp Gly Asp Trp Trp Thr Gly Thr Val Gly Asp	
1025 1030 1035	
aag tcc gga gtc ttc cct tct aac tat gtg agg ctt aaa gat tca	3159
Lys Ser Gly Val Phe Pro Ser Asn Tyr Val Arg Leu Lys Asp Ser	
1040 1045 1050	
gag ggc tct gga act gct ggg aaa aca ggg agt tta gga aaa aaa	3204
Glu Gly Ser Gly Thr Ala Gly Lys Thr Gly Ser Leu Gly Lys Lys	
1055 1060 1065	
cct gaa att gcc cag gtt att gct tcc tac gct gct act ggt ccc	3249
Pro Glu Ile Ala Gln Val Ile Ala Ser Tyr Ala Ala Thr Gly Pro	
1070 1075 1080	
gaa caa ctc acc ctg gct cct ggg cag ctg att ctg atc cgg aaa	3294
Glu Gln Leu Thr Leu Ala Pro Gly Gln Leu Ile Leu Ile Arg Lys	
1085 1090 1095	
aag aac cca ggt gga tgg tgg gaa gga gaa ctg caa gct cga ggg	3339
Lys Asn Pro Gly Gly Trp Trp Glu Gly Glu Leu Gln Ala Arg Gly	
1100 1105 1110	
aaa aag cgc cag ata ggg tgg ttt cca gca aat tat gtc aaa ctt	3384
Lys Lys Arg Gln Ile Gly Trp Phe Pro Ala Asn Tyr Val Lys Leu	
1115 1120 1125	
cta agc ccc gga aca agc aaa atc acc cca act gag cta ccc aag	3429
Leu Ser Pro Gly Thr Ser Lys Ile Thr Pro Thr Glu Leu Pro Lys	
1130 1135 1140	
acc gca gtg cag cca gca gtg tgc cag gtg atc ggg atg tac gat	3474
Thr Ala Val Gln Pro Ala Val Cys Gln Val Ile Gly Met Tyr Asp	
1145 1150 1155	
tac acc gcc cag aac gat gac gaa cta gcc ttc agc aaa ggc cag	3519
Tyr Thr Ala Gln Asn Asp Asp Glu Leu Ala Phe Ser Lys Gly Gln	
1160 1165 1170	
atc atc aac gtc ctc aac aag gag gac ccg gac tgg tgg aaa gga	3564
Ile Ile Asn Val Leu Asn Lys Glu Asp Pro Asp Trp Trp Lys Gly	

1175	1180	1185	
gaa gtc agt ggg caa gtt ggg	ctc ttc cca tcc aat	tat gta aag	3609
Glu Val Ser Gly Gln Val Gly	Leu Phe Pro Ser Asn	Tyr Val Lys	
1190	1195	1200	
ctg acc aca gac atg gac ccc	agc cag caa tga		3642
Leu Thr Thr Asp Met Asp Pro	Ser Gln Gln		
1205	1210		
<210> 3			
<211> 1213			
<212> PRT			
<213> Mus musculus			
<400> 3			
Met Ala Gln Phe Pro Thr Pro Phe Gly Gly Ser Leu Asp Val Trp Ala			
1	5	10	15
Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe Leu Ser Leu			
	20	25	30
Lys Pro Ile Ala Gly Phe Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe			
	35	40	45
Phe Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu			
	50	55	60
Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Val Glu Phe Ser Ile			
65	70	75	80
Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Tyr Gln Leu Pro Ser			
	85	90	95
Thr Leu Pro Pro Val Met Lys Gln Gln Pro Val Ala Ile Ser Ser Ala			
	100	105	110
Pro Ala Phe Gly Ile Gly Gly Ile Ala Ser Met Pro Pro Leu Thr Ala			
	115	120	125
Val Ala Pro Val Pro Met Gly Ser Ile Pro Val Val Gly Met Ser Pro			
	130	135	140
Pro Leu Val Ser Ser Val Pro Pro Ala Ala Val Pro Pro Leu Ala Asn			
145	150	155	160

Gly Ala Pro Pro Val Ile Gln Pro Leu Pro Ala Phe Ala His Pro Ala  
165 170 175

Ala Thr Trp Pro Lys Ser Ser Ser Phe Ser Arg Ser Gly Pro Gly Ser  
180 185 190

Gln Leu Asn Thr Lys Leu Gln Lys Ala Gln Ser Phe Asp Val Ala Ser  
195 200 205

Ala Pro Pro Ala Ala Glu Trp Ala Val Pro Gln Ser Ser Arg Leu Lys  
210 215 220

Tyr Arg Gln Leu Phe Asn Ser His Asp Lys Thr Met Ser Gly His Leu  
225 230 235 240

Thr Gly Pro Gln Ala Arg Thr Ile Leu Met Gln Ser Ser Leu Pro Gln  
245 250 255

Ala Gln Leu Ala Ser Ile Trp Asn Leu Ser Asp Ile Asp Gln Asp Gly  
260 265 270

Lys Leu Thr Ala Glu Glu Phe Ile Leu Ala Met His Leu Ile Asp Val  
275 280 285

Ala Met Ser Gly Gln Pro Leu Pro Pro Val Leu Pro Pro Glu Tyr Ile  
290 295 300

Pro Pro Ser Phe Arg Arg Val Arg Ser Gly Ser Gly Met Ser Val Ile  
305 310 315 320

Ser Ser Ser Ser Val Asp Gln Arg Leu Pro Glu Glu Pro Ser Ser Glu  
325 330 335

Asp Glu Gln Gln Pro Glu Lys Lys Leu Pro Val Thr Phe Glu Asp Lys  
340 345 350

Lys Arg Glu Asn Phe Glu Arg Gly Ser Val Glu Leu Glu Lys Arg Arg  
355 360 365

Gln Ala Leu Leu Glu Gln Gln Arg Lys Glu Gln Glu Arg Leu Ala Gln  
370 375 380

Leu Glu Arg Ala Glu Gln Glu Arg Lys Glu Arg Glu Arg Gln Glu Gln  
 385 390 395 400

Glu Ala Lys Arg Gln Leu Glu Leu Glu Lys Gln Leu Glu Lys Gln Arg  
 405 410 415

Glu Leu Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg  
 420 425 430

Arg Glu Ala Ala Lys Arg Glu Leu Glu Arg Gln Arg Gln Leu Glu Trp  
 435 440 445

Glu Arg Asn Arg Arg Gln Glu Leu Leu Asn Gln Arg Asn Lys Glu Gln  
 450 455 460

Glu Gly Thr Val Val Leu Lys Ala Arg Arg Lys Thr Leu Glu Phe Glu  
 465 470 475 480

Leu Glu Ala Leu Asn Asp Lys Lys His Gln Leu Glu Gly Lys Leu Gln  
 485 490 495

Asp Ile Arg Cys Arg Leu Ala Thr Gln Arg Gln Glu Ile Glu Ser Thr  
 500 505 510

Asn Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln Gln  
 515 520 525

Gln Leu Gln Glu Ser Gln Gln Met Leu Gly Arg Leu Ile Pro Glu Lys  
 530 535 540

Gln Ile Leu Ser Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu His  
 545 550 555 560

Arg Asp Ser Leu Leu Thr Leu Lys Arg Ala Leu Glu Ala Lys Glu Leu  
 565 570 575

Ala Arg Gln Gln Leu Arg Glu Gln Leu Asp Glu Val Glu Arg Glu Thr  
 580 585 590

Arg Ser Lys Leu Gln Glu Ile Asp Val Phe Asn Asn Gln Leu Lys Glu  
 595 600 605

Leu Arg Glu Ile His Ser Lys Gln Gln Leu Gln Lys Gln Arg Ser Leu

610		615		620
Glu Ala Ala Arg Leu Lys Gln Lys Glu Gln Glu Arg Lys Ser Leu Glu				
625		630		635 640
Leu Glu Lys Gln Lys Glu Asp Ala Gln Arg Arg Val Gln Glu Arg Asp				
	645		650	655
Lys Gln Trp Leu Glu His Val Gln Gln Glu Glu Gln Pro Arg Pro Arg				
	660		665	670
Lys Pro His Glu Glu Asp Arg Leu Lys Arg Glu Asp Ser Val Arg Lys				
	675	680		685
Lys Glu Ala Glu Glu Arg Ala Lys Pro Glu Met Gln Asp Lys Gln Ser				
690		695		700
Arg Leu Phe His Pro His Gln Glu Pro Ala Lys Leu Ala Thr Gln Ala				
705		710		715 720
Pro Trp Ser Thr Thr Glu Lys Gly Pro Leu Thr Ile Ser Ala Gln Glu				
	725		730	735
Ser Val Lys Val Val Tyr Tyr Arg Ala Leu Tyr Pro Phe Glu Ser Arg				
	740	745		750
Ser His Asp Glu Ile Thr Ile Gln Pro Gly Asp Ile Val Met Val Asp				
	755	760		765
Glu Ser Gln Thr Gly Glu Pro Gly Trp Leu Gly Gly Glu Leu Lys Gly				
770		775		780
Lys Thr Gly Trp Phe Pro Ala Asn Tyr Ala Glu Lys Ile Pro Glu Asn				
785		790		795 800
Glu Val Pro Thr Pro Ala Lys Pro Val Thr Asp Leu Thr Ser Ala Pro				
	805		810	815
Ala Pro Lys Leu Ala Leu Arg Glu Thr Pro Ala Pro Leu Pro Val Thr				
	820		825	830
Ser Ser Glu Pro Ser Thr Thr Pro Asn Asn Trp Ala Asp Phe Ser Ser				
	835	840		845

Thr Trp Pro Ser Ser Ser Asn Glu Lys Pro Glu Thr Asp Asn Trp Asp  
 850 855 860

Thr Trp Ala Ala Gln Pro Ser Leu Thr Val Pro Ser Ala Gly Gln Leu  
 865 870 875 880

Arg Gln Arg Ser Ala Phe Thr Pro Ala Thr Ala Thr Gly Ser Ser Pro  
 885 890 895

Ser Pro Val Leu Gly Gln Gly Glu Lys Val Glu Gly Leu Gln Ala Gln  
 900 905 910

Ala Leu Tyr Pro Trp Arg Ala Lys Lys Asp Asn His Leu Asn Phe Asn  
 915 920 925

Lys Ser Asp Val Ile Thr Val Leu Glu Gln Gln Asp Met Trp Trp Phe  
 930 935 940

Gly Glu Val Gln Gly Gln Lys Gly Trp Phe Pro Lys Ser Tyr Val Lys  
 945 950 955 960

Leu Ile Ser Gly Pro Val Arg Lys Ser Thr Ser Ile Asp Thr Gly Pro  
 965 970 975

Thr Glu Ser Pro Ala Ser Leu Lys Arg Val Ala Ser Pro Ala Ala Lys  
 980 985 990

Pro Ala Ile Pro Gly Glu Glu Phe Ile Ala Met Tyr Thr Tyr Glu Ser  
 995 1000 1005

Ser Glu Gln Gly Asp Leu Thr Phe Gln Gln Gly Asp Val Ile Val  
 1010 1015 1020

Val Thr Lys Lys Asp Gly Asp Trp Trp Thr Gly Thr Val Gly Asp  
 1025 1030 1035

Lys Ser Gly Val Phe Pro Ser Asn Tyr Val Arg Leu Lys Asp Ser  
 1040 1045 1050

Glu Gly Ser Gly Thr Ala Gly Lys Thr Gly Ser Leu Gly Lys Lys  
 1055 1060 1065

Pro Glu Ile Ala Gln Val Ile Ala Ser Tyr Ala Ala Thr Gly Pro  
1070 1075 1080

Glu Gln Leu Thr Leu Ala Pro Gly Gln Leu Ile Leu Ile Arg Lys  
1085 1090 1095

Lys Asn Pro Gly Gly Trp Trp Glu Gly Glu Leu Gln Ala Arg Gly  
1100 1105 1110

Lys Lys Arg Gln Ile Gly Trp Phe Pro Ala Asn Tyr Val Lys Leu  
1115 1120 1125

Leu Ser Pro Gly Thr Ser Lys Ile Thr Pro Thr Glu Leu Pro Lys  
1130 1135 1140

Thr Ala Val Gln Pro Ala Val Cys Gln Val Ile Gly Met Tyr Asp  
1145 1150 1155

Tyr Thr Ala Gln Asn Asp Asp Glu Leu Ala Phe Ser Lys Gly Gln  
1160 1165 1170

Ile Ile Asn Val Leu Asn Lys Glu Asp Pro Asp Trp Trp Lys Gly  
1175 1180 1185

Glu Val Ser Gly Gln Val Gly Leu Phe Pro Ser Asn Tyr Val Lys  
1190 1195 1200

Leu Thr Thr Asp Met Asp Pro Ser Gln Gln  
1205 1210

<210> 4  
<211> 4625  
<212> DNA  
<213> Mus musculus

<400> 4  
cccttccttt cctttttttg tgttcgctt cggccgtgcc ggctgagagc ccagcagccg 60  
tgacaggctg cgcaacaggt tcgctgcggc cggcctgacg actgaccg cggcggcggc 120  
cgcgccacgg cagggctctt ccggagcttg gccgcgccca cgcgccggtg tcgaggagcg 180  
cgcggggtcg cgccgggacg tgcgcgaggc gccagatggc tgagagctgc aagaagaagt 240  
caggatcatg atggctcagt ttcccacagc gatgaatgga gggccaaata tgtgggctat 300

tacatctgaa gaacgtacta agcatgataa acagtttgat aacctcaaac cttcaggagg	360
ttacataaca ggtgatcaag cccgtacttt tttcctacag tcaggtctgc cggccccggt	420
tttagctgaa atatgggcct tatcagatct gaacaaggat gggaagatgg accagcaaga	480
gttctctata gctatgaaac tcatcaagtt aaagttgcag ggccaacagc tgcctgtagt	540
cctccctcct atcatgaaac aacccctat gttctctcca ctaatctctg ctcgtttttg	600
gatgggaagc atgccaatc tgtccattca tcagccattg cctccagttg cacctatagc	660
aacacccttg tcttctgcta cgtcaggagc cagtattcct cccctaataa tgcctgctcc	720
cctagtgcct tctgttagta catcctcatt accaaatgga actgccagtc tcattcagcc	780
tttatccatt ccttattctt cttcaacatt gcctcatgca tcattcttaca gcctgatgat	840
gggaggattt ggtggtgcta gtatccagaa ggcccagtct ctgattgatt taggatctag	900
tagctcaact tcctcaactg cttccctctc agggaactca cctaagacag ggacctcaga	960
gtgggcagtt cctcagcctt caagattaaa gtatcggcaa aaatttaata gtctagacaa	1020
aggcatgagc ggatacctct caggttttca agctagaaat gcccttcttc agtcaaactc	1080
ctctcaaact cagctagcta ctatttggac tctggctgac atcgatggtg acggacagtt	1140
gaaagctgaa gaatttatct tggcgatgca cctcactgac atggccaaag ctggacagcc	1200
actaccactg acgttgccct ccgagcttgt cctccatct ttcagagggg gaaagcaagt	1260
tgattctgtt aatggaactc tgccttcata tcagaaaaca caagaagaag agcctcagaa	1320
gaaactgcc a gttacttttg aggacaaacg gaaagccaac tatgaacgag gaaacatgga	1380
gctggagaag cgacgccaag tgttgatgga gcagcagcag agggaggctg aacgcaaagc	1440
ccagaaagag aaggaagagt gggagcggaa acagagagaa ctgcaagagc aagaatggaa	1500
gaagcagctg gagttggaga aacgcttgg aaacagaga gagctggaga gacagcggga	1560
ggaagagagg agaaaggaga tagaaagacg agaggcagca aaacaggagc ttgagagaca	1620
acgccgttta gaatgggaaa gactccgtcg gcaggagctg ctcagtcaga agaccaggga	1680
acaagaagac attgtcaggc tgagctccag aaagaaaagt ctccacctgg aactggaagc	1740
agtgaatgga aaacatcagc agatctcagg cagactacaa gatgtccaaa tcagaaagca	1800
aacacaaaag actgagctag aagtttttga taaacagtgt gacctggaaa ttatggaaat	1860
caaacaactt caacaagagc ttaaggaata tcaaaataag cttatctatc tggctccctga	1920
gaagcagcta ttaaacgaaa gaattaaaaa catgcagctc agtaacacac ctgattcagg	1980
gatcagttta cttcataaaa agtcatcaga aaaggaagaa ttatgccaaa gacttaaaga	2040



acaattagat gctcttgaaa aagaaactgc atctaagctc tcagaaatgg attcatttaa	2100
caatcagctg aaggaactca gagaaagcta taatacacag cagttagccc ttgaacaact	2160
tcataaaatc aaacgtgaca aattgaagga aatcgaaaga aaaagattag agcaaattca	2220
aaaaaagaaa ctagaagatg aggctgcaag gaaagcaaag caaggaaaag aaaacttggtg	2280
gagagaaagt attagaaagg aagaagagga aaagcaaaaa cgactccagg aagaaaagtc	2340
acaggacaaa actcaagaag aggaacgaaa agctgaggca aaacaaagtg agacagccag	2400
tgctttgggtg aattacagag cactgtaccc ttttgaagca agaaaccatg atgagatgag	2460
tttttagttct ggggatataa tttaggttga tgaaaaaact gtaggagagc ctgggttggt	2520
ttatggtagt tttcagggaa agtttgggtg gttcccctgc aactatgtag aaaaagtgtc	2580
gtcaagtga aaagctctgt ctcctaagaa ggccttactt cctcctacag tgtctctctc	2640
tgctacctca acttcttccc agccaccagc atcagtgact gattatcaca atgtatcctt	2700
ctcaaactt actgttaata caacatggca gcagaagtca gcttttacc gcactgtgtc	2760
ccctggatct gtgtcccca ttacaggaca ggggcaggct gtagaaaacc tgaaagccca	2820
ggccctttgt tcctggacgg caaagaagga gaaccacctg aacttctcaa agcacgacgt	2880
catcactgtc ctggagcagc aggaaaactg gtggtttggg gaggtgcacg gaggaagagg	2940
atggttcccc aagtcttatg tcaagctcat tcctgggaat gaagtacagc gaggagagcc	3000
agaagctttg tatgcagctg tgactaagaa acctacctcc acagcctatc cagttacctc	3060
cacagcctat ccagttggag aagactacat tgcactttat tcataactcaa gtgtagagcc	3120
cggggatttg actttcactg aaggtgaaga aattctagtg acccagaaag atggagagtg	3180
gtggacagga agtattggag agagaactgg aatcttcccg tccaactacg tcagaccaa	3240
ggatcaagag aattttggga atgctagcaa atctggagca tcaaacaaaa aacccgagat	3300
cgctcaagta acttcagcat atgctgcttc agggactgag cagctcagcc ttgcgccagg	3360
acagttaata ttaatcttaa agaaaaacac aagcgggtgg tggcaaggag agctacaggc	3420
cagaggggaag aaacgacaga agggatggtt tcctgccagc catgtaaagc tgctaggtcc	3480
aagcagtga agaaccatgc ctacttttca cgctgtatgt caagtgattg ctatgtatga	3540
ctacatggcg aataacgaag atgagctcaa tttctccaaa ggacagctga ttaatgttat	3600
gaacaaagat gaccctgact ggtggcaagg agaaaccaat ggtctgactg gtctctttcc	3660
ttcaaactat gttaagatga caacagactc agatccaagt caacagtggg gtgctgaccc	3720

```

ccaagccctg gacacaatgc agcctacgga gaggaagcga cagggctaca ttcacgagct 3780
cattcagaca gaggagcggg acatggacga cctgcaactt tttgaacaaa aaactctcct 3840
ttgagggcct ggggaagcca gaaccagggg agctgcccac aaggctgggt ctaaagacag 3900
at ttgtctct cccaggacag aggagcatca catcggcttc atccatccaa acaagccaca 3960
ctcgtctgggc ctggtatttt attgcaccac taaaattgct agcaatctat gcaaacatga 4020
tctttttaaa caaacgccac agcacagtgc cttgtactag tgttaacctg ttcagctgtg 4080
ttagatgcca gggtttccat tttcagggct ataaaagtat tatgtgggaa atgagacatc 4140
agaccaccgg acgttaccac ttggcaaatc tgtccactgt ggagttgggt atgttggaac 4200
cattccacac tatgtgacct ctgctgggtc acacactcag gaggtgaagg gctgagatga 4260
aatgctgcag ccttggggct tgtgcagcct gatactgaaa tagcatccac ttgtgcactg 4320
aataaataga aacttgatcg ttttattctg actagatatt atcattctct gctaagacaa 4380
tatagtttga aatattatag tttgaatata aggaggaaa cttgatgtac tttaaatata 4440
ctgtgaactc taataatgtg gggatatttt tcaacttta ttttcttaag tataaattat 4500
ttatgtaaat tctttgtttt gcatatttca tagaacatgc atctttaagc tttatcattg 4560
ccaacaatgt acagaaagag aataaaaagta taagtttatg aatgtaaaaa aaaaaaaaaa 4620
aaaaa 4625

```

```

<210> 5
<211> 3594
<212> DNA
<213> Mus musculus

```

```

<220>
<221> CDS
<222> (1)..(3594)
<223> Mouse Ese2

```

```

<400> 5
atg gct cag ttt ccc aca gcg atg aat gga ggg cca aat atg tgg gct 48
Met Ala Gln Phe Pro Thr Ala Met Asn Gly Gly Pro Asn Met Trp Ala
1 5 10 15

att aca tct gaa gaa cgt act aag cat gat aaa cag ttt gat aac ctc 96
Ile Thr Ser Glu Glu Arg Thr Lys His Asp Lys Gln Phe Asp Asn Leu
20 25 30

aaa cct tca gga ggt tac ata aca ggt gat caa gcc cgt act ttt ttc 144
Lys Pro Ser Gly Gly Tyr Ile Thr Gly Asp Gln Ala Arg Thr Phe Phe
35 40 45

```

cta cag tca ggt ctg ccg gcc ccg gtt tta gct gaa ata tgg gcc tta Leu Gln Ser Gly Leu Pro Ala Pro Val Leu Ala Glu Ile Trp Ala Leu 50 55 60	192
tca gat ctg aac aag gat ggg aag atg gac cag caa gag ttc tct ata Ser Asp Leu Asn Lys Asp Gly Lys Met Asp Gln Gln Glu Phe Ser Ile 65 70 75 80	240
gct atg aaa ctc atc aag tta aag ttg cag ggc caa cag ctg cct gta Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Gln Gln Leu Pro Val 85 90 95	288
gtc ctc cct cct atc atg aaa caa ccc cct atg ttc tct cca cta atc Val Leu Pro Pro Ile Met Lys Gln Pro Pro Met Phe Ser Pro Leu Ile 100 105 110	336
tct gct cgt ttt ggg atg gga agc atg ccc aat ctg tcc att cat cag Ser Ala Arg Phe Gly Met Gly Ser Met Pro Asn Leu Ser Ile His Gln 115 120 125	384
cca ttg cct cca gtt gca cct ata gca aca ccc ttg tct tct gct acg Pro Leu Pro Pro Val Ala Pro Ile Ala Thr Pro Leu Ser Ser Ala Thr 130 135 140	432
tca ggg acc agt att cct ccc cta atg atg cct gct ccc cta gtg cct Ser Gly Thr Ser Ile Pro Pro Leu Met Met Pro Ala Pro Leu Val Pro 145 150 155 160	480
tct gtt agt aca tcc tca tta cca aat gga act gcc agt ctc att cag Ser Val Ser Thr Ser Ser Leu Pro Asn Gly Thr Ala Ser Leu Ile Gln 165 170 175	528
cct tta tcc att cct tat tct tct tca aca ttg cct cat gca tca tct Pro Leu Ser Ile Pro Tyr Ser Ser Ser Thr Leu Pro His Ala Ser Ser 180 185 190	576
tac agc ctg atg atg gga gga ttt ggt ggt gct agt atc cag aag gcc Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala 195 200 205	624
cag tct ctg att gat tta gga tct agt agc tca act tcc tca act gct Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Ser Thr Ser Ser Thr Ala 210 215 220	672
tcc ctc tca ggg aac tca cct aag aca ggg acc tca gag tgg gca gtt Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val 225 230 235 240	720
cct cag cct tca aga tta aag tat cgg caa aaa ttt aat agt cta gac Pro Gln Pro Ser Arg Leu Lys Tyr Arg Gln Lys Phe Asn Ser Leu Asp 245 250 255	768
aaa ggc atg agc gga tac ctc tca ggt ttt caa gct aga aat gcc ctt Lys Gly Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu 260 265 270	816
ctt cag tca aat ctc tct caa act cag cta gct act att tgg act ctg	864

Leu	Gln	Ser	Asn	Leu	Ser	Gln	Thr	Gln	Leu	Ala	Thr	Ile	Trp	Thr	Leu	
		275					280					285				
gct	gac	atc	gat	ggt	gac	gga	cag	ttg	aaa	gct	gaa	gaa	ttt	att	ctg	912
Ala	Asp	Ile	Asp	Gly	Asp	Gly	Gln	Leu	Lys	Ala	Glu	Glu	Phe	Ile	Leu	
	290					295				300						
gcg	atg	cac	ctc	act	gac	atg	gcc	aaa	gct	gga	cag	cca	cta	cca	ctg	960
Ala	Met	His	Leu	Thr	Asp	Met	Ala	Lys	Ala	Gly	Gln	Pro	Leu	Pro	Leu	
305					310				315						320	
acg	ttg	cct	ccc	gag	ctt	gtc	cct	cca	tct	ttc	aga	ggg	gga	aag	caa	1008
Thr	Leu	Pro	Pro	Glu	Leu	Val	Pro	Pro	Ser	Phe	Arg	Gly	Gly	Lys	Gln	
				325					330					335		
gtt	gat	tct	gtt	aat	gga	act	ctg	cct	tca	tat	cag	aaa	aca	caa	gaa	1056
Val	Asp	Ser	Val	Asn	Gly	Thr	Leu	Pro	Ser	Tyr	Gln	Lys	Thr	Gln	Glu	
			340				345						350			
gaa	gag	cct	cag	aag	aaa	ctg	cca	gtt	act	ttt	gag	gac	aaa	cgg	aaa	1104
Glu	Glu	Pro	Gln	Lys	Lys	Leu	Pro	Val	Thr	Phe	Glu	Asp	Lys	Arg	Lys	
		355				360					365					
gcc	aac	tat	gaa	cga	gga	aac	atg	gag	ctg	gag	aag	cga	cgc	caa	gtg	1152
Ala	Asn	Tyr	Glu	Arg	Gly	Asn	Met	Glu	Leu	Glu	Lys	Arg	Arg	Gln	Val	
	370					375					380					
ttg	atg	gag	cag	cag	cag	agg	gag	gct	gaa	cgc	aaa	gcc	cag	aaa	gag	1200
Leu	Met	Glu	Gln	Gln	Gln	Arg	Glu	Ala	Glu	Arg	Lys	Ala	Gln	Lys	Glu	
385					390				395						400	
aag	gaa	gag	tgg	gag	cgg	aaa	cag	aga	gaa	ctg	caa	gag	caa	gaa	tgg	1248
Lys	Glu	Glu	Trp	Glu	Arg	Lys	Gln	Arg	Glu	Leu	Gln	Glu	Gln	Glu	Trp	
			405						410					415		
aag	aag	cag	ctg	gag	ttg	gag	aaa	cgc	ttg	gag	aaa	cag	aga	gag	ctg	1296
Lys	Lys	Gln	Leu	Glu	Leu	Glu	Lys	Arg	Leu	Glu	Lys	Gln	Arg	Glu	Leu	
		420					425					430				
gag	aga	cag	cgg	gag	gaa	gag	agg	aga	aag	gag	ata	gaa	aga	cga	gag	1344
Glu	Arg	Gln	Arg	Glu	Glu	Glu	Arg	Arg	Lys	Glu	Ile	Glu	Arg	Arg	Glu	
		435					440					445				
gca	gca	aaa	cag	gag	ctt	gag	aga	caa	cgc	cgt	tta	gaa	tgg	gaa	aga	1392
Ala	Ala	Lys	Gln	Glu	Leu	Glu	Arg	Gln	Arg	Arg	Leu	Glu	Trp	Glu	Arg	
	450					455					460					
ctc	cgt	cgg	cag	gag	ctg	ctc	agt	cag	aag	acc	agg	gaa	caa	gaa	gac	1440
Leu	Arg	Arg	Gln	Glu	Leu	Leu	Ser	Gln	Lys	Thr	Arg	Glu	Gln	Glu	Asp	
465					470					475					480	
att	gtc	agg	ctg	agc	tcc	aga	aag	aaa	agt	ctc	cac	ctg	gaa	ctg	gaa	1488
Ile	Val	Arg	Leu	Ser	Ser	Arg	Lys	Lys	Ser	Leu	His	Leu	Glu	Leu	Glu	
				485					490					495		
gca	gtg	aat	gga	aaa	cat	cag	cag	atc	tca	ggc	aga	cta	caa	gat	gtc	1536
Ala	Val	Asn	Gly	Lys	His	Gln	Gln	Ile	Ser	Gly	Arg	Leu	Gln	Asp	Val	

500	505	510	
caa atc aga aag caa aca caa aag act gag cta gaa gtt ttg gat aaa Gln Ile Arg Lys Gln Thr Gln Lys Thr Glu Leu Glu Val Leu Asp Lys 515 520 525			1584
cag tgt gac ctg gaa att atg gaa atc aaa caa ctt caa caa gag ctt Gln Cys Asp Leu Glu Ile Met Glu Ile Lys Gln Leu Gln Gln Glu Leu 530 535 540			1632
aag gaa tat caa aat aag ctt atc tat ctg gtc cct gag aag cag cta Lys Glu Tyr Gln Asn Lys Leu Ile Tyr Leu Val Pro Glu Lys Gln Leu 545 550 555 560			1680
tta aac gaa aga att aaa aac atg cag ctc agt aac aca cct gat tca Leu Asn Glu Arg Ile Lys Asn Met Gln Leu Ser Asn Thr Pro Asp Ser 565 570 575			1728
ggg atc agt tta ctt cat aaa aag tca tca gaa aag gaa gaa tta tgc Gly Ile Ser Leu Leu His Lys Lys Ser Ser Glu Lys Glu Glu Leu Cys 580 585 590			1776
caa aga ctt aaa gaa caa tta gat gct ctt gaa aaa gaa act gca tct Gln Arg Leu Lys Glu Gln Leu Asp Ala Leu Glu Lys Glu Thr Ala Ser 595 600 605			1824
aag ctc tca gaa atg gat tca ttt aac aat cag ctg aag gaa ctc aga Lys Leu Ser Glu Met Asp Ser Phe Asn Asn Gln Leu Lys Glu Leu Arg 610 615 620			1872
gaa agc tat aat aca cag cag tta gcc ctt gaa caa ctt cat aaa atc Glu Ser Tyr Asn Thr Gln Gln Leu Ala Leu Glu Gln Leu His Lys Ile 625 630 635 640			1920
aaa cgt gac aaa ttg aag gaa atc gaa aga aaa aga tta gag caa att Lys Arg Asp Lys Leu Lys Glu Ile Glu Arg Lys Arg Leu Glu Gln Ile 645 650 655			1968
caa aaa aag aaa cta gaa gat gag gct gca agg aaa gca aag caa gga Gln Lys Lys Lys Leu Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly 660 665 670			2016
aaa gaa aac ttg tgg aga gaa agt att aga aag gaa gaa gag gaa aag Lys Glu Asn Leu Trp Arg Glu Ser Ile Arg Lys Glu Glu Glu Glu Lys 675 680 685			2064
caa aaa cga ctc cag gaa gaa aag tca cag gac aaa act caa gaa gag Gln Lys Arg Leu Gln Glu Glu Lys Ser Gln Asp Lys Thr Gln Glu Glu 690 695 700			2112
gaa cga aaa gct gag gca aaa caa agt gag aca gcc agt gct ttg gtg Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val 705 710 715 720			2160
aat tac aga gca ctg tac cct ttt gaa gca aga aac cat gat gag atg Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met 725 730 735			2208

agt ttt agt tct ggg gat ata att cag gtt gat gaa aaa act gta gga	2256
Ser Phe Ser Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly	
740 745 750	
gag cct ggt tgg ctt tat ggt agt ttt cag gga aag ttt ggc tgg ttc	2304
Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe	
755 760 765	
ccc tgc aac tat gta gaa aaa gtg ctg tca agt gaa aaa gct ctg tct	2352
Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser	
770 775 780	
cct aag aag gcc tta ctt cct cct aca gtg tct ctc tct gct acc tca	2400
Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser	
785 790 795 800	
act tct tcc cag cca cca gca tca gtg act gat tat cac aat gta tcc	2448
Thr Ser Ser Gln Pro Pro Ala Ser Val Thr Asp Tyr His Asn Val Ser	
805 810 815	
ttc tca aac ctt act gtt aat aca aca tgg cag cag aag tca gct ttt	2496
Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe	
820 825 830	
acc cgc act gtg tcc cct gga tct gtg tcc ccc att cac gga cag ggg	2544
Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly	
835 840 845	
cag gct gta gaa aac ctg aaa gcc cag gcc ctt tgt tcc tgg acg gca	2592
Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala	
850 855 860	
aag aag gag aac cac ctg aac ttc tca aag cac gac gtc atc act gtc	2640
Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val	
865 870 875 880	
ctg gag cag cag gaa aac tgg tgg ttt ggg gag gtg cac gga gga aga	2688
Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg	
885 890 895	
gga tgg ttc ccc aag tct tat gtc aag ctc att cct ggg aat gaa gta	2736
Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val	
900 905 910	
cag cga gga gag cca gaa gct ttg tat gca gct gtg act aag aaa cct	2784
Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro	
915 920 925	
acc tcc aca gcc tat cca gtt acc tcc aca gcc tat cca gtt gga gaa	2832
Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu	
930 935 940	
gac tac att gca ctt tat tca tac tca agt gta gag ccc ggg gat ttg	2880
Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Ser Val Glu Pro Gly Asp Leu	
945 950 955 960	

act ttc act gaa ggt gaa gaa att cta gtg acc cag aaa gat gga gag	2928
Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys Asp Gly Glu	
965 970 975	
tgg tgg aca gga agt att gga gag aga act gga atc ttc ccg tcc aac	2976
Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn	
980 985 990	
tac gtc aga cca aag gat caa gag aat ttt ggg aat gct agc aaa tct	3024
Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser	
995 1000 1005	
gga gca tca aac aaa aaa ccc gag atc gct caa gta act tca gca	3069
Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala	
1010 1015 1020	
tat gct gct tca ggg act gag cag ctc agc ctt gcg cca gga cag	3114
Tyr Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln	
1025 1030 1035	
tta ata tta atc tta aag aaa aac aca agc ggg tgg tgg caa gga	3159
Leu Ile Leu Ile Leu Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly	
1040 1045 1050	
gag cta cag gcc aga ggg aag aaa cga cag aag gga tgg ttt cct	3204
Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Lys Gly Trp Phe Pro	
1055 1060 1065	
gcc agc cat gta aag ctg cta ggt cca agc agt gaa aga acc atg	3249
Ala Ser His Val Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met	
1070 1075 1080	
cct act ttt cac gct gta tgt caa gtg att gct atg tat gac tac	3294
Pro Thr Phe His Ala Val Cys Gln Val Ile Ala Met Tyr Asp Tyr	
1085 1090 1095	
atg gcg aat aac gaa gat gag ctc aat ttc tcc aaa gga cag ctg	3339
Met Ala Asn Asn Glu Asp Glu Leu Asn Phe Ser Lys Gly Gln Leu	
1100 1105 1110	
att aat gtt atg aac aaa gat gac cct gac tgg tgg caa gga gaa	3384
Ile Asn Val Met Asn Lys Asp Asp Pro Asp Trp Trp Gln Gly Glu	
1115 1120 1125	
acc aat ggt ctg act ggt ctc ttt cct tca aac tat gtt aag atg	3429
Thr Asn Gly Leu Thr Gly Leu Phe Pro Ser Asn Tyr Val Lys Met	
1130 1135 1140	
aca aca gac tca gat cca agt caa cag tgg tgt gct gac ctc caa	3474
Thr Thr Asp Ser Asp Pro Ser Gln Gln Trp Cys Ala Asp Leu Gln	
1145 1150 1155	
gcc ctg gac aca atg cag cct acg gag agg aag cga cag ggc tac	3519
Ala Leu Asp Thr Met Gln Pro Thr Glu Arg Lys Arg Gln Gly Tyr	
1160 1165 1170	
att cac gag ctc att cag aca gag gag cgg tac atg gac gac ctg	3564

Ile His Glu Leu Ile Gln Thr Glu Glu Arg Tyr Met Asp Asp Leu  
 1175 1180 1185

caa ctt ttt gaa caa aaa act ctc ctt tga  
 Gln Leu Phe Glu Gln Lys Thr Leu Leu  
 1190 1195

3594

<210> 6  
 <211> 1197  
 <212> PRT  
 <213> Mus musculus

<400> 6

Met Ala Gln Phe Pro Thr Ala Met Asn Gly Gly Pro Asn Met Trp Ala  
 1 5 10 15

Ile Thr Ser Glu Glu Arg Thr Lys His Asp Lys Gln Phe Asp Asn Leu  
 20 25 30

Lys Pro Ser Gly Gly Tyr Ile Thr Gly Asp Gln Ala Arg Thr Phe Phe  
 35 40 45

Leu Gln Ser Gly Leu Pro Ala Pro Val Leu Ala Glu Ile Trp Ala Leu  
 50 55 60

Ser Asp Leu Asn Lys Asp Gly Lys Met Asp Gln Gln Glu Phe Ser Ile  
 65 70 75 80

Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Gln Gln Leu Pro Val  
 85 90 95

Val Leu Pro Pro Ile Met Lys Gln Pro Pro Met Phe Ser Pro Leu Ile  
 100 105 110

Ser Ala Arg Phe Gly Met Gly Ser Met Pro Asn Leu Ser Ile His Gln  
 115 120 125

Pro Leu Pro Pro Val Ala Pro Ile Ala Thr Pro Leu Ser Ser Ala Thr  
 130 135 140

Ser Gly Thr Ser Ile Pro Pro Leu Met Met Pro Ala Pro Leu Val Pro  
 145 150 155 160

Ser Val Ser Thr Ser Ser Leu Pro Asn Gly Thr Ala Ser Leu Ile Gln  
 165 170 175



Pro Leu Ser Ile Pro Tyr Ser Ser Ser Thr Leu Pro His Ala Ser Ser  
180 185 190

Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala  
195 200 205

Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Ser Thr Ser Ser Thr Ala  
210 215 220

Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val  
225 230 235 240

Pro Gln Pro Ser Arg Leu Lys Tyr Arg Gln Lys Phe Asn Ser Leu Asp  
245 250 255

Lys Gly Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu  
260 265 270

Leu Gln Ser Asn Leu Ser Gln Thr Gln Leu Ala Thr Ile Trp Thr Leu  
275 280 285

Ala Asp Ile Asp Gly Asp Gly Gln Leu Lys Ala Glu Glu Phe Ile Leu  
290 295 300

Ala Met His Leu Thr Asp Met Ala Lys Ala Gly Gln Pro Leu Pro Leu  
305 310 315 320

Thr Leu Pro Pro Glu Leu Val Pro Pro Ser Phe Arg Gly Gly Lys Gln  
325 330 335

Val Asp Ser Val Asn Gly Thr Leu Pro Ser Tyr Gln Lys Thr Gln Glu  
340 345 350

Glu Glu Pro Gln Lys Lys Leu Pro Val Thr Phe Glu Asp Lys Arg Lys  
355 360 365

Ala Asn Tyr Glu Arg Gly Asn Met Glu Leu Glu Lys Arg Arg Gln Val  
370 375 380

Leu Met Glu Gln Gln Gln Arg Glu Ala Glu Arg Lys Ala Gln Lys Glu  
385 390 395 400

Lys Glu Glu Trp Glu Arg Lys Gln Arg Glu Leu Gln Glu Gln Glu Trp  
405 410 415

Lys Lys Gln Leu Glu Leu Glu Lys Arg Leu Glu Lys Gln Arg Glu Leu  
420 425 430

Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg Arg Glu  
435 440 445

Ala Ala Lys Gln Glu Leu Glu Arg Gln Arg Arg Leu Glu Trp Glu Arg  
450 455 460

Leu Arg Arg Gln Glu Leu Leu Ser Gln Lys Thr Arg Glu Gln Glu Asp  
465 470 475 480

Ile Val Arg Leu Ser Ser Arg Lys Lys Ser Leu His Leu Glu Leu Glu  
485 490 495

Ala Val Asn Gly Lys His Gln Gln Ile Ser Gly Arg Leu Gln Asp Val  
500 505 510

Gln Ile Arg Lys Gln Thr Gln Lys Thr Glu Leu Glu Val Leu Asp Lys  
515 520 525

Gln Cys Asp Leu Glu Ile Met Glu Ile Lys Gln Leu Gln Gln Glu Leu  
530 535 540

Lys Glu Tyr Gln Asn Lys Leu Ile Tyr Leu Val Pro Glu Lys Gln Leu  
545 550 555 560

Leu Asn Glu Arg Ile Lys Asn Met Gln Leu Ser Asn Thr Pro Asp Ser  
565 570 575

Gly Ile Ser Leu Leu His Lys Lys Ser Ser Glu Lys Glu Glu Leu Cys  
580 585 590

Gln Arg Leu Lys Glu Gln Leu Asp Ala Leu Glu Lys Glu Thr Ala Ser  
595 600 605

Lys Leu Ser Glu Met Asp Ser Phe Asn Asn Gln Leu Lys Glu Leu Arg  
610 615 620

Glu Ser Tyr Asn Thr Gln Gln Leu Ala Leu Glu Gln Leu His Lys Ile  
625 630 635 640

Lys Arg Asp Lys Leu Lys Glu Ile Glu Arg Lys Arg Leu Glu Gln Ile  
645 650 655

Gln Lys Lys Lys Leu Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly  
660 665 670

Lys Glu Asn Leu Trp Arg Glu Ser Ile Arg Lys Glu Glu Glu Glu Lys  
675 680 685

Gln Lys Arg Leu Gln Glu Glu Lys Ser Gln Asp Lys Thr Gln Glu Glu  
690 695 700

Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val  
705 710 715 720

Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met  
725 730 735

Ser Phe Ser Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly  
740 745 750

Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe  
755 760 765

Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser  
770 775 780

Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser  
785 790 795 800

Thr Ser Ser Gln Pro Pro Ala Ser Val Thr Asp Tyr His Asn Val Ser  
805 810 815

Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe  
820 825 830

Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly  
835 840 845

Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala

850		855		860
Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val				
865		870		875 880
Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg				
	885		890	895
Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val				
	900		905	910
Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro				
	915		920	925
Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu				
	930		935	940
Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Ser Val Glu Pro Gly Asp Leu				
	945		950	955 960
Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys Asp Gly Glu				
	965		970	975
Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn				
	980		985	990
Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser				
	995		1000	1005
Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala				
	1010		1015	1020
Tyr Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln				
	1025		1030	1035
Leu Ile Leu Ile Leu Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly				
	1040		1045	1050
Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Lys Gly Trp Phe Pro				
	1055		1060	1065
Ala Ser His Val Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met				
	1070		1075	1080

Pro Thr Phe His Ala Val Cys Gln Val Ile Ala Met Tyr Asp Tyr  
1085 1090 1095

Met Ala Asn Asn Glu Asp Glu Leu Asn Phe Ser Lys Gly Gln Leu  
1100 1105 1110

Ile Asn Val Met Asn Lys Asp Asp Pro Asp Trp Trp Gln Gly Glu  
1115 1120 1125

Thr Asn Gly Leu Thr Gly Leu Phe Pro Ser Asn Tyr Val Lys Met  
1130 1135 1140

Thr Thr Asp Ser Asp Pro Ser Gln Gln Trp Cys Ala Asp Leu Gln  
1145 1150 1155

Ala Leu Asp Thr Met Gln Pro Thr Glu Arg Lys Arg Gln Gly Tyr  
1160 1165 1170

Ile His Glu Leu Ile Gln Thr Glu Glu Arg Tyr Met Asp Asp Leu  
1175 1180 1185

Gln Leu Phe Glu Gln Lys Thr Leu Leu  
1190 1195

<210> 7  
<211> 738  
<212> DNA  
<213> Mus musculus

<400> 7  
ccgtcttcca catttccac attgatcgtg tgtacacact ccgaacagac aacatcaacg 60  
agaggacggc ctgggtccag aagatcaagg gtgcctcaga gcagtacatc gacactgaga 120  
agaagaaacg ggaaaaggct taccaagccc gttctcaaaa gacttcaggt attgggcgtc 180  
tgatggtgca tgtcattgaa gctacagaat taaaagcctg caaaccaaac gggaaaagta 240  
atccatactg tgaagtcagc atgggctccc aaagctatac caccaggacc ctgcaggaca 300  
cactaaaccc caagtggaac ttcaactgcc agttcttcat caaggatctt taccaggacg 360  
ttctgtgtct cactatgttt gacagagacc agttttctcc agatgacttc ttgggtcgta 420  
ctgaagttcc agtggcaaaa atccgaacag aacaggaaaag caaaggcccc accacccgcc 480  
gactactact gcacgaagtc cccactggag aagtctgggt ccgctttgac ctgcaacttt 540

ttgaacaaaa aactctcctt tgagggcctg gggaagccag aaccagggga gctgcccaca 600  
aggctgggtc taaagacaga ttttgctctc ccaggacaga ggagcatcac atggcttcat 660  
ccatcaaaca gccacactcg ctgggcctgt attttattgc acactaaatt gctagcaatc 720  
tatgcaaaca tgatcttt 738

<210> 8  
<211> 186  
<212> PRT  
<213> Mus musculus

<400> 8

Val Phe His Ile Ser His Ile Asp Arg Val Tyr Thr Leu Arg Thr Asp  
1 5 10 15

Asn Ile Asn Glu Arg Thr Ala Trp Val Gln Lys Ile Lys Gly Ala Ser  
20 25 30

Glu Gln Tyr Ile Asp Thr Glu Lys Lys Lys Arg Glu Lys Ala Tyr Gln  
35 40 45

Ala Arg Ser Gln Lys Thr Ser Gly Ile Gly Arg Leu Met Val His Val  
50 55 60

Ile Glu Ala Thr Glu Leu Lys Ala Cys Lys Pro Asn Gly Lys Ser Asn  
65 70 75 80

Pro Tyr Cys Glu Val Ser Met Gly Ser Gln Ser Tyr Thr Thr Arg Thr  
85 90 95

Leu Gln Asp Thr Leu Asn Pro Lys Trp Asn Phe Asn Cys Gln Phe Phe  
100 105 110

Ile Lys Asp Leu Tyr Gln Asp Val Leu Cys Leu Thr Met Phe Asp Arg  
115 120 125

Asp Gln Phe Ser Pro Asp Asp Phe Leu Gly Arg Thr Glu Val Pro Val  
130 135 140

Ala Lys Ile Arg Thr Glu Gln Glu Ser Lys Gly Pro Thr Thr Arg Arg  
145 150 155 160

Leu Leu Leu His Glu Val Pro Thr Gly Glu Val Trp Val Arg Phe Asp  
165 170 175

Leu Gln Leu Phe Glu Gln Lys Thr Leu Leu  
180 185

<210> 9  
<211> 1078  
<212> DNA  
<213> Mus musculus

<400> 9  
gaattcggca cgagggctga gagaagcggg ctccgaggac tctgatgctg aagagaagcc 60  
tgttaagcag gaggacttcc cgaagattta ggaccaaaga agttaagac gggtaggcaat 120  
ttaaagccca gccagaaagg cttttcagga ggaaccaagt ctttcatgga ctttggcagc 180  
tgaggagagac acacgaaagg gatcgggcag aagctgctgc agaagatggg ctacgtccct 240  
gggcgtggcc tggggaagaa cgcacagggg atcatcaacc ccatcgaagc caaacagaga 300  
aaaggcaagg gagccgtggg ggcctatggc tcggagagga cactcagtc tctgcaggac 360  
ttccccgtgg ccgactcgga agaggaggca gaagaggagt ttcagaagga gctgagccaa 420  
tgaggagaaag accccagcgg gagcaagaag aagccaaagt actcttaca gactgtggag 480  
gagctgaagg ccaagggcag ggtcagcaag aagctcacag cacctcagaa ggaactgtct 540  
caggtcaagg tgatcgacat gacaggccgg gagcagaagg tgtactacag ctacagccaa 600  
atcagccaca agcacagcgt gcccgatgaa ggggtgccat tgctggcgca gctgcccccc 660  
acagccggca aggaagccag gatgccgggc ttgactctgc ctgagctgga gcacaacctg 720  
cagctgctca ttgagcgac ggagcaggag atcatccaga gcgaccggca gctccagtat 780  
gagcgggaca tggtagtcag cctgtcgcat gagctggaga agacggccga ggttcttgca 840  
catgaggagc gtgtcatctc taacctcagc aaggtgctgg ccctgggtgga ggaatgtgag 900  
cgccgcatgc agcccatgg caccgacccc ctactctgg atgagtgtgc ccgcatcttt 960  
gagacactac aggacaagta ttatgaggag taccgcctgg cggaccgcgc agacctcgct 1020  
gtggccattg tctaccgct cgtgaaggac tactttaagg attggcacc ctcgaggg 1078

<210> 10  
<211> 309  
<212> PRT  
<213> Mus musculus

<400> 10

Gly	Thr	Lys	Ser	Phe	Met	Asp	Phe	Gly	Ser	Trp	Glu	Arg	His	Thr	Lys	1	5	10	15
Gly	Ile	Gly	Gln	Lys	Leu	Leu	Gln	Lys	Met	Gly	Tyr	Val	Pro	Gly	Arg	20	25	30	
Gly	Leu	Gly	Lys	Asn	Ala	Gln	Gly	Ile	Ile	Asn	Pro	Ile	Glu	Ala	Lys	35	40	45	
Gln	Arg	Lys	Gly	Lys	Gly	Ala	Val	Gly	Ala	Tyr	Gly	Ser	Glu	Arg	Thr	50	55	60	
Thr	Gln	Ser	Leu	Gln	Asp	Phe	Pro	Val	Ala	Asp	Ser	Glu	Glu	Glu	Ala	65	70	75	80
Glu	Glu	Glu	Phe	Gln	Lys	Glu	Leu	Ser	Gln	Trp	Arg	Lys	Asp	Pro	Ser	85	90	95	
Gly	Ser	Lys	Lys	Lys	Pro	Lys	Tyr	Ser	Tyr	Lys	Thr	Val	Glu	Glu	Leu	100	105	110	
Lys	Ala	Lys	Gly	Arg	Val	Ser	Lys	Lys	Leu	Thr	Ala	Pro	Gln	Lys	Glu	115	120	125	
Leu	Ser	Gln	Val	Lys	Val	Ile	Asp	Met	Thr	Gly	Arg	Glu	Gln	Lys	Val	130	135	140	
Tyr	Tyr	Ser	Tyr	Ser	Gln	Ile	Ser	His	Lys	His	Ser	Val	Pro	Asp	Glu	145	150	155	160
Gly	Val	Pro	Leu	Leu	Ala	Gln	Leu	Pro	Pro	Thr	Ala	Gly	Lys	Glu	Ala	165	170	175	
Arg	Met	Pro	Gly	Phe	Ala	Leu	Pro	Glu	Leu	Glu	His	Asn	Leu	Gln	Leu	180	185	190	
Leu	Ile	Glu	Arg	Thr	Glu	Gln	Glu	Ile	Ile	Gln	Ser	Asp	Arg	Gln	Leu	195	200	205	
Gln	Tyr	Glu	Arg	Asp	Met	Val	Val	Ser	Leu	Ser	His	Glu	Leu	Glu	Lys	210	215	220	



Thr Ala Glu Val Leu Ala His Glu Glu Arg Val Ile Ser Asn Leu Ser  
 225 230 235 240

Lys Val Leu Ala Leu Val Glu Glu Cys Glu Arg Arg Met Gln Pro His  
 245 250 255

Gly Thr Asp Pro Leu Thr Leu Asp Glu Cys Ala Arg Ile Phe Glu Thr  
 260 265 270

Leu Gln Asp Lys Tyr Tyr Glu Glu Tyr Arg Leu Ala Asp Arg Ala Asp  
 275 280 285

Leu Ala Val Ala Ile Val Tyr Pro Leu Val Lys Asp Tyr Phe Lys Asp  
 290 295 300

Trp His Pro Ser Arg  
 305

<210> 11  
 <211> 97  
 <212> DNA  
 <213> Mus musculus

<400> 11  
 catggcggcg gctgcggagg gcgtcccggc gacgcgaacgg aggacgagcc acctcgagat 60  
 gatgctgcgg tggagacagc cgaggaagca aaggagc 97

<210> 12  
 <211> 123  
 <212> DNA  
 <213> Mus musculus

<400> 12  
 cttgagtcta ctgaaaatac cctgcaggaa gctacatcat ccatgtcttt gatgacccaa 60  
 tttgaacagg aagtatctgg cctccaaaga ccatactga tattgagact agcgaagaga 120  
 tgc 123

<210> 13  
 <211> 140  
 <212> DNA  
 <213> Mus musculus

<400> 13  
 gaattcggca cgagggagtc tggttctgga aagccgacag aagctgagct tgtcaactta 60  
 gatttcttgg gagatttggga tggtccggta tctgccccac ccctgtgtgt ctgagctcga 120

gtctctctgc tggactatgg 140

<210> 14  
 <211> 2855  
 <212> DNA  
 <213> Mus musculus

<400> 14  
 ctttacgagc agagggagcc aaattcagag ccgttttaga taaagctgtg caagcggatg 60  
 gacagggtgaa ggagcgctac cagtcccatc gagacaccat cgcacttctg tgtaagccgg 120  
 agccagagct gaatgctgcc atccccctctg ctaaccacgc aaagaccatg cagggcagcg 180  
 aggttgtaag tgtcttaaag tccttattat caaatcttga tgaaatcaag aaggaaagag 240  
 agagtcttga gaatgacctg aagtcagtga attttgacat gacaagcaag tttttgacag 300  
 ctctggccca agatggcgtg ataaatgagg aggctctctc tgtcactgag ctggatcgga 360  
 tctatggcgg tctaacaagt aaagttcaag agtctctgaa gaaacaagag ggacttctaa 420  
 aaaatataca ggtctcacac caagaattct ccaaaatgaa gcaatctaac aacgaggcta 480  
 acttgagaga agaagttctg aagaacctag caactgcgta tgacaacttt gttgagcttg 540  
 tagctaactt gaaggagggc acaaagtttt acaatgagct gactgagatc ctgggtcaggt 600  
 tccagaacaa atgcagtgac atagtgtttg cacggaagac agaaagagac gagctcttga 660  
 aggatctgca gcagagcatt gccagagagc ccagcgctcc ttcaatccct cctccagcct 720  
 atcagtcctc ccagcagcg gggcatgcag cagcgctcc aactccagcc ccaagaacca 780  
 tgccgcctgc taagccccag cctccagccc ggcctccacc tctgtgctt cctgcaaacc 840  
 gagttcctcc tgcttctgct gctgctgccc ctgcaggcgt ggggacggct tcagcagcgc 900  
 cgccacagac ccctggctct gctccccgc cacaggctca gggaccacca taccctacct 960  
 atccaggata tcccgggtat tgccaaatgc ccatgcccac gggctacaac ccctacgcat 1020  
 atggccagta caatatgccg taccaccggt tgtatcacca gagccccgga cagggtccat 1080  
 acccaggacc ccagcagcct acctaccct tccctcagcc cccgcagcag tcctactatc 1140  
 cacagcagta acgctgccac gtgctgctgg ttcagatcag agcgacagga cagcagctgc 1200  
 caccagctct aagccacgct ctggccactc gagagtatct tgctctattg attgctgtgg 1260  
 atgatttctg tctgtggcta aagccgaagg ctggggccca cctccacatt tgatcgact 1320  
 cgtgagattc tgctgctgtt gcagtataaa cgtagctat aatagcattt gaaaaaatt 1380  
 acagttccat aaaatgctga aaatgagaaa ttaaacctgc aagtgaacaa tttgaaatta 1440

gcatacttta taagatgcag ttgggacaaa gatggcttaa gtactgatat ttaaggaaaa	1500
agttttcttt ctcttttggg ttattgattt agtttaattt ctattatgat attttgcata	1560
atcaaggcat tgtaaatctt ataatttaaa aataaattac ttacgaacag ttgtcattgt	1620
tatgttttgt cattgattct cattgctgtc tagttccttt ctggtattag cctctccttc	1680
tgtatgttca caggctccat tactgtgttg aattgctga cgtcagggtga gcagtcaggg	1740
agggtgctc tgcggacgcc aagcgcacac cagcttgtct caggctcagc agtcagctca	1800
tctggacatt tctatttaaa agtcctttaa tgtggaagat acacacaatt gttaccaaaag	1860
gttcttccaa ttaattttac aatttaaaaa gtatgtatta atgttttatt gttagatttt	1920
ccaaaaaaat gatgcaaatt ctggtaatat tcatttcctt caccataat ttggttaaaa	1980
tgagtagttt tagccataca gtctcatctg ctgtggagga acctggagaa agtccccctgt	2040
gcctttctag cccttgggtt ctattcttat cctgcaatgt ctactgcaca gtgtgtttga	2100
gcagatccta accctccttt tacagtttct tcttcttact tctttattct ttttgtggct	2160
cctgaaatct gaggttattt tgtaattcag gagcatgcag gacaattgtt gggacatgtg	2220
cctagtccgg aatacagccc aggacagcaa ggagatgcgt cctgcaccag gaagccgtgc	2280
aggcaggagc tgtccaaggc cccggcggct ctgcctgtgt gaggcaggag aatgagcaga	2340
ttccctaate tatgttctcg aagtttaatg ctgatgttgt cttgccttat cctcatttaa	2400
ctgatactgt caccagtcac acctttgtct tcattgcaaa gtgatagtgt aatttcaa	2460
gtaagactga agatacgatt gtaaaagga gtaaaactgg ttaaactgtt tattctaaag	2520
caccttactt tgttgttgta tgcagaaaac acagatgcgc taattcagta taaatgactg	2580
attgcctgga atttggacgt tggcttaaaag tccgatagct aaaccttggc aaaacataac	2640
aaacatttca ttgctcagcc tcagtgtctt ggagtattca gtgtatgaga caggtttatt	2700
tgagtcctct gtaaattgca tttgaatttt atattctccc ctcccagta tcttataaga	2760
catcccctga gttaggaggt tcccagactg ctactctatt ccttatgaat gcaaaacaac	2820
caccaataga acaaaaaaaaa aaaaaaaaaac tcgag	2855

<210> 15  
 <211> 1151  
 <212> DNA  
 <213> Mus musculus

<400> 15	
ctttacgagc agaggagacc aaattcagag ccgttttaga taaagctgtg caagcggatg	60

gacaggtgaa ggagcgctac cagtcccatc gagacacccat cgcacttctg tgtaagccgg 120  
agccagagct gaatgctgcc atccccctctg ctaaccacagc aaagaccatg cagggcagcg 180  
aggttgtaag tgtcttaaag tccttattat caaatcttga tgaaatcaag aaggaaagag 240  
agagtcttga gaatgacctg aagtcagtga attttgacat gacaagcaag tttttgacag 300  
ctctggccca agatggcgtg ataaatgagg aggctctctc tgtcactgag ctggatcggg 360  
tctatggcgg tctaacaagt aaagttcaag agtctctgaa gaaacaagag ggacttctaa 420  
aaaatataca ggtctcacac caagaattct ccaaaatgaa gcaatctaac aacgaggcta 480  
acttgagaga agaagttctg aagaacctag caactgcgta tgacaacttt gttgagcttg 540  
tagctaactt gaaggagggc acaaagtttt acaatgagct gactgagatc ctggtcaggt 600  
tccagaacaa atgcagtgc atagtgtttg cacggaagac agaaagagac gagctcttga 660  
aggatctgca gcagagcatt gccagagagc ccagcgcctc ttcaatccct cctccagcct 720  
atcagtcttc cccagcagcg gggcatgcag cagcgcctcc aactccagcc ccaagaacca 780  
tgccgcctgc taagccccag cctccagccc ggccctccacc tcctgtgctt cctgcaaacc 840  
gagttcctcc tgcttctgct gctgctgccc ctgcaggcgt ggggacggct tcagcagcgc 900  
cgccacagac ccctggctct gctccccgc cacaggctca gggaccacca taccctacct 960  
atccaggata tcccgggtat tgccaaatgc ccattgccc atggctacaac ccctacgcat 1020  
atggccagta caatatgccg taccacccgg tgtatcacca gagccccgga caggctccat 1080  
acccaggacc ccagcagcct acctaccct tccctcagcc cccgcagcag tcctactatc 1140  
cacagcagta a 1151

<210> 16  
<211> 382  
<212> PRT  
<213> Mus musculus

<400> 16

Leu Arg Ala Glu Gly Ala Lys Phe Arg Ala Val Leu Asp Lys Ala Val  
1 5 10 15

Gln Ala Asp Gly Gln Val Lys Glu Arg Tyr Gln Ser His Arg Asp Thr  
20 25 30

Ile Ala Leu Leu Cys Lys Pro Glu Pro Glu Leu Asn Ala Ala Ile Pro  
35 40 45

Ser Ala Asn Pro Ala Lys Thr Met Gln Gly Ser Glu Val Val Ser Val  
 50 55 60

Leu Lys Ser Leu Leu Ser Asn Leu Asp Glu Ile Lys Lys Glu Arg Glu  
 65 70 75 80

Ser Leu Glu Asn Asp Leu Lys Ser Val Asn Phe Asp Met Thr Ser Lys  
 85 90 95

Phe Leu Thr Ala Leu Ala Gln Asp Gly Val Ile Asn Glu Glu Ala Leu  
 100 105 110

Ser Val Thr Glu Leu Asp Arg Ile Tyr Gly Gly Leu Thr Ser Lys Val  
 115 120 125

Gln Glu Ser Leu Lys Lys Gln Glu Gly Leu Leu Lys Asn Ile Gln Val  
 130 135 140

Ser His Gln Glu Phe Ser Lys Met Lys Gln Ser Asn Asn Glu Ala Asn  
 145 150 155 160

Leu Arg Glu Glu Val Leu Lys Asn Leu Ala Thr Ala Tyr Asp Asn Phe  
 165 170 175

Val Glu Leu Val Ala Asn Leu Lys Glu Gly Thr Lys Phe Tyr Asn Glu  
 180 185 190

Leu Thr Glu Ile Leu Val Arg Phe Gln Asn Lys Cys Ser Asp Ile Val  
 195 200 205

Phe Ala Arg Lys Thr Glu Arg Asp Glu Leu Leu Lys Asp Leu Gln Gln  
 210 215 220

Ser Ile Ala Arg Glu Pro Ser Ala Pro Ser Ile Pro Pro Pro Ala Tyr  
 225 230 235 240

Gln Ser Ser Pro Ala Ala Gly His Ala Ala Ala Pro Pro Thr Pro Ala  
 245 250 255

Pro Arg Thr Met Pro Pro Ala Lys Pro Gln Pro Pro Ala Arg Pro Pro  
 260 265 270

Pro Pro Val Leu Pro Ala Asn Arg Val Pro Pro Ala Ser Ala Ala Ala  
 275 280 285

Ala Pro Ala Gly Val Gly Thr Ala Ser Ala Ala Pro Pro Gln Thr Pro  
 290 295 300

Gly Ser Ala Pro Pro Pro Gln Ala Gln Gly Pro Pro Tyr Pro Thr Tyr  
 305 310 315 320

Pro Gly Tyr Pro Gly Tyr Cys Gln Met Pro Met Pro Met Gly Tyr Asn  
 325 330 335

Pro Tyr Ala Tyr Gly Gln Tyr Asn Met Pro Tyr Pro Pro Val Tyr His  
 340 345 350

Gln Ser Pro Gly Gln Ala Pro Tyr Pro Gly Pro Gln Gln Pro Thr Tyr  
 355 360 365

Pro Phe Pro Gln Pro Pro Gln Gln Ser Tyr Tyr Pro Gln Gln  
 370 375 380

<210> 17  
 <211> 1738  
 <212> DNA  
 <213> Mus musculus

<400> 17  
 ggtcttggtc agaatttttaa atttcttctc atttgagtaa aatgttgcac tctgaagtcc 60  
 catgctacct gaagttgcac ttggagtccc aagctactgg aatgtttata tgtgaccgtt 120  
 tcccaggagg cttacactgc agaaggaaga atgaatctag gtgaggtggg cagctgcttg 180  
 gcagtcctct cttgtgcccc aactgtaaac cagatagaaa tggtcagggg aggatacttt 240  
 cattattgtg gttttagtag ttaagatgat tgcttctgcc ttggaaatac ctcaagctgt 300  
 tcttatttaa caggtaagtg actgagtata atattccaga aaaatttgaa atcctaattt 360  
 cttccatatt tcattaaatt ttttgcatac aggtctaaca aatatggata tgtatacaca 420  
 tcctctttta tgaaggtatt attttgggta cttttcctaa gatatacctt aaaagatggt 480  
 ctatacattt cctacttaaa ttctggggga ttggagtat gtacatgata aaaaagatta 540  
 taatatatcg attgaagtta ctttattttt taattagaat tattttaata gtcctttatt 600  
 gaataagtgc tgtaatttgt ttgctatgag acttattcct gatgtgaatg taaattattt 660

ttccacatgc atgaaaaaat gtatgtacta atcagagttg tctccattgc attgaaatta	720
cttgttttga actaaagtaa ctcatattta tgtagtagaa tgcttatgtt ttcagacttt	780
gtaatgattt cctttggatg tatttttaa atcaatcggtct gggtaacata tcagtttaga	840
ttaatatgtg cttaaaagaa gaaaaaaatt caatggttca tagtagaaat gtgccacact	900
taaataagct ctgtatgaca tgaaattctg ttaaaacatt gtaattcatg gtgactttta	960
acttataaaa atactacttg cacgggttac ttgatttatg gatatatgaa aacttctcag	1020
gacgaaagtt cttctttctc tagaactatt cttctgtcgg tcatgcagaa tgctgttatt	1080
ctgaaaagtg tccctgttgc atatgatggt cactttattt ggggggattc ttcataagat	1140
gtgagatgtt gatgccagtc tttcccaagt aagtgtcgt aaaaaaggac tactaactag	1200
cctgcatctg tctctaactg ggaccaaggg gtctgtctgaa ggaaactgaa gagctctaac	1260
attttcacag cttggagaag atagaatctt taaaagtaca actgaagctt gatctatttt	1320
acaagtgc atgatggccc tgctcttctc tggttcctgt catttgaaac caactcctgt	1380
tgtaaatagg aagaatatgg gacattcata ttaagaaaaa tttgatgtca ttaggtgact	1440
aagtagaagg cttagaaaaa tgtattcatt tgcaagtatt ttggcacaag aaattttcca	1500
actgaatagt aagcaaaagc taagttgttt cattgaaatc ataaggcagt ttaagataaa	1560
ctggagaaga taactgttct aatagaggat aatcgaattg attgtcaagt ggatgttatt	1620
tattggatag tgacagagtt tatttgtaac cttaattata ttaaaagtta ttctgttagg	1680
atgttttgta ttaataaacg tgaacaaaat taaaaaaaaa aaaaaaaaaa ctcgaggg	1738

<210> 18  
 <211> 1521  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> misc\_feature  
 <222> (102)..(103)  
 <223> "n" represents any nucleotide.

<400> 18	
gagaaggcgg cctgccgcag cgggacaacc tagagcgcga cgtggaggcg cgtagcggag	60
ctggagcaac tgcgcaccga ggtggatgtg cgcattagcg cnntggacac ctgcgtcaag	120
gccaaagtcgc tgccagccgt cccgccgaga gtctcaggcc ccccccgaa ccctccaccc	180
attgatccag ctagcctgga ggaattcaag aaaaggatcc tggagtctca gcggctccct	240

gtagtcaacc	ctgcwgccca	accagcggt	tgagracca	gctgccgcag	gacgctgggt	300
gccagaatcg	cccacctgtg	gatgggggca	gccaggtgcc	cacagtgtctg	gacacccgcc	360
gtgcctgccg	gcagcctcca	ccccagcgc	cttctctggc	accccttcac	tgtcccstgc	420
atccccrcca	ttcsscasws	askggattta	aggcacacac	agctgtgaga	tgacttcaca	480
tcgaccctt	gtgcagtgc	ccggatggg	ccccaccac	acatgaagca	cccacagctc	540
agctgccacc	ctaggcaact	cctccggttt	cctatcactc	tgctcctgac	ccgggagggtg	600
agaacaggaa	gccagcctt	cagctccctt	gggagtttcc	agcctccctc	ttaaaggcca	660
ctagggtttc	cagatcctat	ttgagagtct	ccaggcctcc	cctgaagggt	tctagccacc	720
acgcccacag	gattccatt	aggttttaaa	gtcttttcca	gagtccgctg	gttccccctc	780
tcctcacaag	gaagggcctc	aattgtagat	gagcgttccg	ggtggatctt	agagccctag	840
agggaggctt	ttgcttgtar	ccccctaaag	atattactgg	cacataataa	atatgaaagt	900
cctttgaaag	ttggacactg	cgcaaagg	gctctccatg	gaccgcagcc	catacgccc	960
cacgggggac	cagcagcgcg	gctctggttc	tacctgcgct	atttcttct	cttcgtgtcg	1020
ctcattcagt	tcctcatcat	cctgggcctg	gtcctcttca	tgatctatgg	caatgtgcac	1080
gccaccactg	agtccagcct	gcgcgccacg	gagatccgcg	ccgacagcct	gtacagccag	1140
gtggttgga	tatcggcctc	acaggctaac	ctgagcaaac	agctgaacat	cagcttgctt	1200
gtcaaggaaa	cagtcatgca	gcaactgttg	actacgcgac	gtgagatgga	gcgcatcaac	1260
gccagcttcc	gccagtcca	aggcgacctg	atcacctaca	taaactataa	tcgcttcac	1320
gccgctatca	tcctgagcga	gaagcagtgc	caggaacagc	tgaaggaggt	caacaagacc	1380
tgcgaaacttt	actcttcaag	ctgggagaaa	aagttaagac	actggagatg	gagggtggcca	1440
aggagaaggc	agtgtgctcc	aaggacaagg	agagcctgct	ggcaggaaag	cggcagacgg	1500
aagagcagct	ggaggcctgt	g				1521

<210> 19  
 <211> 720  
 <212> DNA  
 <213> Mus musculus

<400> 19	
tgtgcgccgc	ctctagaact agtggatccc ccgggcctgc aggaattccg gcacgacggc 60
cgagcgccgc	ggaccacccg cggctgccc ccgagccgctc gacatgtggg gggactgggg 120
tgggagcggc	cggagcagcg ccaggtagcc gggcgcgag aaccatggct ctcgctcgcc 180



tgctctgacc	tggcttgctc	gccccaccga	agaatgtcag	ccaagtccaa	ggggaaccct	240
cctcgtcctc	cgcagccgag	ggaccgccgg	cagcctccaa	aaccaagggtg	aaggagcaga	300
tcaagatcat	agtggaggat	ctggaattag	tcctgggcga	cctgaaggac	gtggccaaaag	360
aacttaagga	ggtggttgac	cagattgaca	ccctgacctc	tgatctacag	ctggaagatg	420
agatgaccga	cagctccaaa	acagacactc	tgaacagcag	ctccagtggg	acaacagcct	480
ccagcataga	gaagatcaaa	gaacaggcca	atgctcccct	cattaaacct	ccagcacacc	540
cgtctgctat	cctgactgtc	ctgagaaaagc	caaaccctcc	accgcctcct	ccaagggttga	600
cacccgtgag	gtgtgaagag	cctcagagag	tggtgccgac	tgccaaccct	gtaaaagacca	660
atggcactct	tctgcggaat	ggaggcttag	cggggaggcc	caacaaaatt	ccaaatggag	720

<210> 20  
 <211> 801  
 <212> DNA  
 <213> Mus musculus

<400> 20						
ctcgagtttt	tttttttttt	tttttttttt	tttcattatt	tactattatt	tattgacata	60
tttccaaagc	tcaaaatatt	ttattataca	tatagttgaa	catatgtttc	aaattgtata	120
gtatagaaaa	taaacttttt	tgtagtgtcc	tcagcatttc	atgatgcaa	actattgaca	180
aacatcttta	gaaaaataat	aaaatagtcc	ttcgggtatta	aaattcttat	taaaaagcat	240
tagatcaaag	ggagaactat	gacatcatca	atgcatagat	gagataggca	tgaatggaat	300
gagttgccct	ggcttttatca	acaaatcaaa	atatctgaca	tcccagctct	tataatagac	360
caaaatactt	ggaatcagaa	ggtcacagtt	tgtttttaggt	caatcacaaa	aaaataaaat	420
tcattcatac	tttctcaatt	ttccgcagtt	tctgatgatg	gaacatagaa	aacaatgtac	480
gtccaggaca	gaggcgctac	tctgcatact	taccacgtga	ttttttatgc	cactttgttg	540
aatgcagatt	aatatatttg	ggctttttat	tgcttgagta	gaaagtgctc	attacttatt	600
attttacggt	tatcatatag	aaaattaaaa	acaaacagaa	cgttttctta	aatggcagat	660
atcacactgt	ggtagtggtg	gatttcctca	ggatggctct	ctgtggtttt	ggtgcagcgg	720
gaggaggcac	ggttgcagggt	gtgggagggg	ggaaaactgtt	actgtggctt	attcccagtc	780
ccccattttc	taatgggaaa	t				801

<210> 21  
 <211> 119  
 <212> DNA

<213> Mus musculus

<400> 21

gcacagcccc cctccatcct gaagaaaacc tcagcgtatg ggccctccagc ttcggggccgt 60

gtctatcctt cctctcctgg gacatggtgt tccccgcttg cccccctggc agaaaaccg 119

<210> 22

<211> 5738

<212> DNA

<213> Mus musculus

<400> 22

cggcacgagg aggagtggag cggcgcgggg agggcgcgca gcttggttgc tccgtagtac 60

ggcggctcgc aaggagcat cccgagcggg ctccgggacg gccgggaggc aggcaggcgg 120

gcgggcgggg atggtgtgcy cggctgcgga ctccggcgtt ctgcgcggc gtgcgggctg 180

cactgatttg tgtgaggggc ggccgcgcgc acccgcccgg agatgaggcg tcgatcagca 240

aggatgaacgt aatagaacca tggctcagtt tcccacacct ttcggtggta gcctggatgt 300

ctgggccata actgtggagg aaagggccaa gcatgaccag cagttcctta gcctgaagcc 360

gatagcggga ttattactg gtgatcaagc gaggaacttt tttttccaat ctgggttacc 420

tcagcctgtc ttagcacaaa tatgggcgct agcggacatg aataacgatg gaaggatgga 480

tcaagtggaa ttttccatag ccatgaagct tatcaaactg aagctadaag gatatcagct 540

ccccccaca cttccccctg tcatgaaaca gcaaccagtg gctatttcca gtgcaccagc 600

atttggtata ggagggattg ctagcatgcc accactcaca gctgttgctc ctgtgccaat 660

gggctccatt ccagttgttg gaatgtctcc acccttagta tcttctgtcc ctccagcagc 720

agtgcctccc ctggctaacg gggctcctcc cgtcatacag cctctgcctg cgtttgcgca 780

tctgcagcc acatggccaa agagtcttc cttcagcaga tctggtccag ggtcacaatt 840

aaacactaag ttacagaagg cacaatcatt cgatgtcgcc agcgcccctc cagcagcaga 900

atgggctgtg cctcagtcatt caaggctgaa atacaggcag ttattcaaca gccacgacaa 960

aactatgagt ggacacttaa caggccccca ggcaagaact attctcatgc aatcaagttt 1020

acccagggt cagctggctt caatatggaa tctttctgac attgatcaag atggaaaact 1080

cactgcagaa gaatttatcc tagctatgca cctaattgat gttgccatgt ctggtcagcc 1140

actgccgcc gtctgcctc cagaatacat cctccttcc ttcagaagag ttcgctccgg 1200

cagtgggatg tccgtcataa gctcttcttc tgtggatcag aggctgcctg aggagccgtc 1260

gtcagaggat gagcagcagc cagagaagaa actgcctgtg acatttgaag ataagaagcg 1320

ggagaacttc gagcgaggca gtgtggagct ggagaagcgc cggcaagcgc tcttggagca	1380
gcagcgcaaa gagcaggagc ggttggctca gctggagcgc gccgagcagg agaggaaaga	1440
gcgggagcgc caggagcagg aggccaagcg gcagctggag ctggagaagc agctggagaa	1500
gcagcgggag ctggagcggc agcgagagga ggagaggagg aaggagatcg agaggcgcga	1560
ggccgcaaaa cgggaactgg aaaggcagcg acaacttgaa tgggaacgga accggagaca	1620
ggaactcctg aatcagagga acaaggagca ggagggcacc gtggtcctga aggcaaggag	1680
gaagactctg gagttttagt tagaagctct gaatgacaaa aagcatcagc tagaaggaaa	1740
acttcaggat atcaggtgtc gactggcaac ccagaggcaa gaaattgaga gcacgaacaa	1800
gtctagagag ctaagaattg ctgaaatcac ccacttacag cagcagttgc aggaatctca	1860
gcaaatgctt ggaagactta ttccagagaa acagatactc agtgaccagt taaaacaagt	1920
ccagcagaac agtttgcata gagactcgct tcttaccctc aaaagagcct tggaagcaaa	1980
ggagctggcc cggcagcagc tccgggagca gctggacgag gtggagagag agaccaggtc	2040
aaagctgcag gagattgatg ttttcaacaa ccagctgaag gaactgagag agatacatag	2100
caaacagcaa ctccagaagc agaggtccct ggaggcagcg cgactgaagc agaaagagca	2160
ggagaggaag agcctggagt tagagaagca aaaggaagac gctcagagac gagttcagga	2220
aagggacaag caatggctgg agcatgtgca gcaggaggag cagccacgcc cccggaaacc	2280
ccacgaggag gacagactga agaggggaaga cagtgtcagg aagaaggagg cggaagagag	2340
agccaagccg gaaatgcaag acaagcagag tcggcttttc catccgcac aggagccagc	2400
taagctggcc acccaggcac cctggtctac cacagagaaa ggcccgtta ccatttctgc	2460
acaggagagt gtaaaagtgg tatattaccg agcgctgtac ccctttgaat ccagaagtca	2520
cgatgagatc accatccagc caggagatat agtcatggtg gatgaaagcc agactggaga	2580
gccaggatgg cttggaggag agctgaaagg gaagacggga tggttccctg caaactatgc	2640
agaaaagatt ccagaaaatg aggttccac tccagccaaa ccagtgaccg atctgacatc	2700
tgcccctgcc cccaaactgg ctctgcgtga gaccctgct cctttgccag tgacctcttc	2760
tgagccctcc acaaccccca acaactgggc agacttcagt tccacgtggc ccagcagctc	2820
aaacgagaag ccagaaacgg acaactggga tacgtgggcg gctcagcctt ctctgaccgt	2880
acctagtgtc ggccagttac ggagagatc agcctttacc ccagccacag ccactggctc	2940
ctccccatct cccgtcctgg gccagggtga aaagggtgaa gggctacaag cgcaagccct	3000

gtatccctgg agagccaaaa aagacaacca cttaaatttt aacaaaagtg acgtcatcac 3060  
 cgttctggaa cagcaagaca tgtggtggtt tggagaagtt caaggtcaga agggttggtt 3120  
 cccaagtct tacgtgaaac tcatttcagg gcccgtaagg aaatccacaa gcatcgatac 3180  
 tggccctact gaaagtcctg ctagtctaaa gagagtggct tccccggccg ccaagccagc 3240  
 cattccccga gaagagttta ttgccatgta cacatacgag agttctgagc aaggagattt 3300  
 aacctttcag caaggggatg tgattgtggt taccaagaaa gatggtgact ggtggacggg 3360  
 aacggtgggc gacaagtccg gagtcttccc ttctaactat gtgaggctta aagattcaga 3420  
 gggctctgga actgctggga aaacagggag tttaggaaaa aaacctgaaa ttgccagggt 3480  
 tattgcttcc tacgtgcta ctggtcccg acaactcacc ctggctcctg ggcagctgat 3540  
 tctgatccgg aaaaagaacc caggtggatg gtgggaagga gaactgcaag ctcgagggaa 3600  
 aaagcgccag ataggggtgt ttccagcaaa ttatgtcaaa cttctaagcc ccggaacaag 3660  
 caaatcacc ccaactgagc taccgaagac cgcagtgcag ccagcagtgt gccagggtgat 3720  
 cgggatgtac gattacaccg ccagaacga tgacgaacta gccttcagca aaggccagat 3780  
 catcaacgtc ctcaacaagg aggaccgga ctggtggaaa ggagaagtca gtgggcaagt 3840  
 tgggtctctc ccatccaatt atgtaaagct gaccacagac atggaccca gccagcaatg 3900  
 gtgctcagac ctgcatctct tagatatgct gaccccgact gagaggaagc ggcaaggcta 3960  
 catccatgaa ctcatgtca cggaggagaa ctacgtgaac gacttgagc tggtcacaga 4020  
 gatctttcag aaaccctga cggagtctga gctgctgaca gaaaaagagg ttgctatgat 4080  
 ttttgtaac tggaaggagc tgatcatgtg taatatcaaa ctgctgaaag cgctgagagt 4140  
 ccgcaagaag atgtctgggg agaagatgcc ggtgaagatg attggcgaca tcctgagcgc 4200  
 ccagctgccg cacatgcagc cttacatccg cttctgcagc tgccagctca atggggctgc 4260  
 cctcatccag cagaagacgg acgaggctcc agacttcaag gagttcgtca aaagactggc 4320  
 aatggaccct cggtgcaaag gaatgcctct gtccagcttt atactgaagc ctatgcagcg 4380  
 tgtcacaaga taccgctga tcattaaaaa catcctggaa aacactcctg agaaccatcc 4440  
 agaccacagc cacctgaagc atgccctgga aaaggcggag gagctgtgct ccaggtgaa 4500  
 cgagggagtt cgagagaagg agaactcaga ccggctggag tggatccaag ccacgtgca 4560  
 gtgtgaaggc ctttctgagc aactggtgtt caattcagt accaactgct tgggaccacg 4620  
 caagtttctg cacagcggga agctctacaa ggccaagagc aataaagaac tgtatggctt 4680  
 cctcttcaac gacttcctcc tgctgacca aatcaciaag cccttaggct cttccggcac 4740

```

cgacaaagtc ttcagcccca aatctaacct tcagtataaa atgtacaaaa cgcccatttt 4800
cttaaagttag gttctagtaa aattgcccac ggacccttct ggagatgagc ctatcttcca 4860
catttcccac atcgaccggg tctacacctt ccgagcagag agcataaatg agaggactgc 4920
ctgggtgcag aaaatcaagg cggcgtctga gctctacata gagacggaga aaaagaagcg 4980
agagaaggcg tacctggtcc gttcccagcg ggcgaccggt attggaaggt tgatggtgaa 5040
cgtggtagaa ggcattgagc tgaagccctg tcggtcacat ggaaagagca acccgtagtg 5100
tgaggtagacc atgggctctc agtgccacat caccaagaca atccaggaca cgctaaaccc 5160
caagtggaat tctaactgcc agttcttcat cagagacctg gagcaggagg ttctctgcat 5220
cacagtgttt gagagggacc agttctcgcc tgatgatttt ttgggtcgga cagagatccg 5280
agtggccgac atcaagaaag accagggctc caaggggccc gttacgaagt gtctcctgct 5340
gcatgaggtc cccacgggag agattgtggt ccgccttgac ctgcagttgt ttgatgagcc 5400
gtagcagccc tgcgatgac gtagatgact tctctctcaa ggccccgtgc gggcgtgctg 5460
tctggtggtc agcctcagag caacggggat gaagcaaaga cgaagcccct cgaggctgct 5520
aggagtcggt ctcgacaatc ctgcccttca aaccatgtct cattttatga atccaaattc 5580
tcttttcctt tgctctccct atgggtctcat catggcttct agagtctctg aaatctgtga 5640
cctttaacta ggttccattg ggagcctggc tccttccttg ggctggagggt gtgggtctgg 5700
tttctataaa atagattata aactcgagaa tcactagt 5738

```

```

<210> 23
<211> 5145
<212> DNA
<213> Mus musculus

```

```

<220>
<221> CDS
<222> (1) .. (5145)
<223> Mouse EseiL

```

```

<400> 23
atg gct cag ttt ccc aca cct ttc ggt ggt agc ctg gat gtc tgg gcc 48
Met Ala Gln Phe Pro Thr Pro Phe Gly Gly Ser Leu Asp Val Trp Ala
1 5 10 15
ata act gtg gag gaa agg gcc aag cat gac cag cag ttc ctt agc ctg 96
Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe Leu Ser Leu
20 25 30
aag ccg ata gcg gga ttt att act ggt gat caa gcg agg aac ttt ttt 144

```

Lys	Pro	Ile	Ala	Gly	Phe	Ile	Thr	Gly	Asp	Gln	Ala	Arg	Asn	Phe	Phe		
		35					40					45					
ttc	caa	tct	ggg	tta	cct	cag	cct	gtc	tta	gca	caa	ata	tgg	gcg	cta	192	
Phe	Gln	Ser	Gly	Leu	Pro	Gln	Pro	Val	Leu	Ala	Gln	Ile	Trp	Ala	Leu		
	50					55				60							
gcg	gac	atg	aat	aac	gat	gga	agg	atg	gat	caa	gtg	gaa	ttt	tcc	ata	240	
Ala	Asp	Met	Asn	Asn	Asp	Gly	Arg	Met	Asp	Gln	Val	Glu	Phe	Ser	Ile		
65					70					75					80		
gcc	atg	aag	ctt	atc	aaa	ctg	aag	cta	caa	gga	tat	cag	ctc	ccc	tcc	288	
Ala	Met	Lys	Leu	Ile	Lys	Leu	Lys	Leu	Gln	Gly	Tyr	Gln	Leu	Pro	Ser		
				85				90						95			
aca	ctt	ccc	cct	gtc	atg	aaa	cag	caa	cca	gtg	gct	att	tcc	agt	gca	336	
Thr	Leu	Pro	Pro	Val	Met	Lys	Gln	Gln	Pro	Val	Ala	Ile	Ser	Ser	Ala		
			100				105						110				
cca	gca	ttt	ggt	ata	gga	ggg	att	gct	agc	atg	cca	cca	ctc	aca	gct	384	
Pro	Ala	Phe	Gly	Ile	Gly	Gly	Ile	Ala	Ser	Met	Pro	Pro	Leu	Thr	Ala		
		115					120					125					
gtt	gct	cct	gtg	cca	atg	ggc	tcc	att	cca	gtt	gtt	gga	atg	tct	cca	432	
Val	Ala	Pro	Val	Pro	Met	Gly	Ser	Ile	Pro	Val	Val	Gly	Met	Ser	Pro		
	130					135					140						
ccc	tta	gta	tct	tct	gtc	cct	cca	gca	gca	gtg	cct	ccc	ctg	gct	aac	480	
Pro	Leu	Val	Ser	Ser	Val	Pro	Pro	Ala	Ala	Val	Pro	Pro	Leu	Ala	Asn		
145					150					155					160		
ggg	gct	cct	ccc	gtc	ata	cag	cct	ctg	cct	gcg	ttt	gcg	cat	cct	gca	528	
Gly	Ala	Pro	Pro	Val	Ile	Gln	Pro	Leu	Pro	Ala	Phe	Ala	His	Pro	Ala		
				165				170						175			
gcc	aca	tgg	cca	aag	agt	tct	tcc	ttc	agc	aga	tct	ggt	cca	ggg	tca	576	
Ala	Thr	Trp	Pro	Lys	Ser	Ser	Ser	Phe	Ser	Arg	Ser	Gly	Pro	Gly	Ser		
			180					185					190				
caa	tta	aac	act	aag	tta	cag	aag	gca	caa	tca	ttc	gat	gtc	gcc	agc	624	
Gln	Leu	Asn	Thr	Lys	Leu	Gln	Lys	Ala	Gln	Ser	Phe	Asp	Val	Ala	Ser		
		195					200					205					
gcc	cct	cca	gca	gca	gaa	tgg	gct	gtg	cct	cag	tca	tca	agg	ctg	aaa	672	
Ala	Pro	Pro	Ala	Ala	Glu	Trp	Ala	Val	Pro	Gln	Ser	Ser	Arg	Leu	Lys		
	210					215					220						
tac	agg	cag	tta	ttc	aac	agc	cac	gac	aaa	act	atg	agt	gga	cac	tta	720	
Tyr	Arg	Gln	Leu	Phe	Asn	Ser	His	Asp	Lys	Thr	Met	Ser	Gly	His	Leu		
225					230					235					240		
aca	ggt	ccc	cag	gca	aga	act	att	ctc	atg	caa	tca	agt	tta	ccc	cag	768	
Thr	Gly	Pro	Gln	Ala	Arg	Thr	Ile	Leu	Met	Gln	Ser	Ser	Leu	Pro	Gln		
				245				250						255			
gct	cag	ctg	gct	tca	ata	tgg	aat	ctt	tct	gac	att	gat	caa	gat	gga	816	
Ala	Gln	Leu	Ala	Ser	Ile	Trp	Asn	Leu	Ser	Asp	Ile	Asp	Gln	Asp	Gly		

260										265										270										
aaa	ctc	act	gca	gaa	gaa	ttt	atc	cta	gct	atg	cac	cta	att	gat	gtt	864														
Lys	Leu	Thr	Ala	Glu	Glu	Phe	Ile	Leu	Ala	Met	His	Leu	Ile	Asp	Val															
275						280						285																		
gcc	atg	tct	ggg	cag	cca	ctg	ccg	ccc	gtc	ctg	cct	cca	gaa	tac	atc	912														
Ala	Met	Ser	Gly	Gln	Pro	Leu	Pro	Pro	Val	Leu	Pro	Pro	Glu	Tyr	Ile															
290			295						300																					
cct	cct	tcc	ttc	aga	aga	gtt	cgc	tcc	ggc	agt	ggg	atg	tcc	gtc	ata	960														
Pro	Pro	Ser	Phe	Arg	Arg	Val	Arg	Ser	Gly	Ser	Gly	Met	Ser	Val	Ile															
305			310						315						320															
agc	tct	tct	tct	gtg	gat	cag	agg	ctg	cct	gag	gag	ccg	tcg	tca	gag	1008														
Ser	Ser	Ser	Ser	Val	Asp	Gln	Arg	Leu	Pro	Glu	Glu	Pro	Ser	Ser	Glu															
325						330						335																		
gat	gag	cag	cag	cca	gag	aag	aaa	ctg	cct	gtg	aca	ttt	gaa	gat	aag	1056														
Asp	Glu	Gln	Gln	Pro	Glu	Lys	Lys	Leu	Pro	Val	Thr	Phe	Glu	Asp	Lys															
340						345						350																		
aag	cgg	gag	aac	ttc	gag	cga	ggc	agt	gtg	gag	ctg	gag	aag	cgc	cgg	1104														
Lys	Arg	Glu	Asn	Phe	Glu	Arg	Gly	Ser	Val	Glu	Leu	Glu	Lys	Arg	Arg															
355				360						365																				
caa	gcg	ctc	ttg	gag	cag	cag	cgc	aaa	gag	cag	gag	cgg	ttg	gct	cag	1152														
Gln	Ala	Leu	Leu	Glu	Gln	Gln	Arg	Lys	Glu	Gln	Glu	Arg	Leu	Ala	Gln															
370				375						380																				
ctg	gag	cgc	gcc	gag	cag	gag	agg	aaa	gag	cgg	gag	cgc	cag	gag	cag	1200														
Leu	Glu	Arg	Ala	Glu	Gln	Glu	Arg	Lys	Glu	Arg	Glu	Arg	Gln	Glu	Gln															
385			390						395						400															
gag	gcc	aag	cgg	cag	ctg	gag	ctg	gag	aag	cag	ctg	gag	aag	cag	cgg	1248														
Glu	Ala	Lys	Arg	Gln	Leu	Glu	Leu	Glu	Lys	Gln	Leu	Glu	Lys	Gln	Arg															
405						410						415																		
gag	ctg	gag	cgg	cag	cga	gag	gag	gag	agg	agg	aag	gag	atc	gag	agg	1296														
Glu	Leu	Glu	Arg	Gln	Arg	Glu	Glu	Glu	Arg	Arg	Lys	Glu	Ile	Glu	Arg															
420						425						430																		
cgc	gag	gcc	gca	aaa	cgg	gaa	ctg	gaa	agg	cag	cga	caa	ctt	gaa	tgg	1344														
Arg	Glu	Ala	Ala	Lys	Arg	Glu	Leu	Glu	Arg	Gln	Arg	Gln	Leu	Glu	Trp															
435				440						445																				
gaa	cgg	aac	cgg	aga	cag	gaa	ctc	ctg	aat	cag	agg	aac	aag	gag	cag	1392														
Glu	Arg	Asn	Arg	Arg	Gln	Glu	Leu	Leu	Asn	Gln	Arg	Asn	Lys	Glu	Gln															
450				455						460																				
gag	ggc	acc	gtg	gtc	ctg	aag	gca	agg	agg	aag	act	ctg	gag	ttt	gag	1440														
Glu	Gly	Thr	Val	Val	Leu	Lys	Ala	Arg	Arg	Lys	Thr	Leu	Glu	Phe	Glu															
465			470						475						480															
tta	gaa	gct	ctg	aat	gac	aaa	aag	cat	cag	cta	gaa	gga	aaa	ctt	cag	1488														
Leu	Glu	Ala	Leu	Asn	Asp	Lys	Lys	His	Gln	Leu	Glu	Gly	Lys	Leu	Gln															
485						490						495																		

gat atc agg tgt cga ctg gca acc cag agg caa gaa att gag agc acg	1536
Asp Ile Arg Cys Arg Leu Ala Thr Gln Arg Gln Glu Ile Glu Ser Thr	
500 505 510	
aac aag tct aga gag cta aga att gct gaa atc acc cac tta cag cag	1584
Asn Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln Gln	
515 520 525	
cag ttg cag gaa tct cag caa atg ctt gga aga ctt att cca gag aaa	1632
Gln Leu Gln Glu Ser Gln Gln Met Leu Gly Arg Leu Ile Pro Glu Lys	
530 535 540	
cag ata ctc agt gac cag tta aaa caa gtc cag cag aac agt ttg cat	1680
Gln Ile Leu Ser Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu His	
545 550 555 560	
aga gac tcg ctt ctt acc ctc aaa aga gcc ttg gaa gca aag gag ctg	1728
Arg Asp Ser Leu Leu Thr Leu Lys Arg Ala Leu Glu Ala Lys Glu Leu	
565 570 575	
gcc cgg cag cag ctc cgg gag cag ctg gac gag gtg gag aga gag acc	1776
Ala Arg Gln Gln Leu Arg Glu Gln Leu Asp Glu Val Glu Arg Glu Thr	
580 585 590	
agg tca aag ctg cag gag att gat gtt ttc aac aac cag ctg aag gaa	1824
Arg Ser Lys Leu Gln Glu Ile Asp Val Phe Asn Asn Gln Leu Lys Glu	
595 600 605	
ctg aga gag ata cat agc aaa cag caa ctc cag aag cag agg tcc ctg	1872
Leu Arg Glu Ile His Ser Lys Gln Gln Leu Gln Lys Gln Arg Ser Leu	
610 615 620	
gag gca gcg cga ctg aag cag aaa gag cag gag agg aag agc ctg gag	1920
Glu Ala Ala Arg Leu Lys Gln Lys Glu Gln Glu Arg Lys Ser Leu Glu	
625 630 635 640	
tta gag aag caa aag gaa gac gct cag aga cga gtt cag gaa agg gac	1968
Leu Glu Lys Gln Lys Glu Asp Ala Gln Arg Arg Val Gln Glu Arg Asp	
645 650 655	
aag caa tgg ctg gag cat gtg cag cag gag gag cag cca cgc ccc cgg	2016
Lys Gln Trp Leu Glu His Val Gln Gln Glu Glu Gln Pro Arg Pro Arg	
660 665 670	
aaa ccc cac gag gag gac aga ctg aag agg gaa gac agt gtc agg aag	2064
Lys Pro His Glu Glu Asp Arg Leu Lys Arg Glu Asp Ser Val Arg Lys	
675 680 685	
aag gag gcg gaa gag aga gcc aag ccg gaa atg caa gac aag cag agt	2112
Lys Glu Ala Glu Glu Arg Ala Lys Pro Glu Met Gln Asp Lys Gln Ser	
690 695 700	
cgg ctt ttc cat ccg cat cag gag cca gct aag ctg gcc acc cag gca	2160
Arg Leu Phe His Pro His Gln Glu Pro Ala Lys Leu Ala Thr Gln Ala	
705 710 715 720	



ccc tgg tct acc aca gag aaa ggc ccg ctt acc att tct gca cag gag	2208
Pro Trp Ser Thr Thr Glu Lys Gly Pro Leu Thr Ile Ser Ala Gln Glu	
725 730 735	
agt gta aaa gtg gta tat tac cga gcg ctg tac ccc ttt gaa tcc aga	2256
Ser Val Lys Val Val Tyr Tyr Arg Ala Leu Tyr Pro Phe Glu Ser Arg	
740 745 750	
agt cac gat gag atc acc atc cag cca gga gat ata gtc atg gtg gat	2304
Ser His Asp Glu Ile Thr Ile Gln Pro Gly Asp Ile Val Met Val Asp	
755 760 765	
gaa agc cag act gga gag cca gga tgg ctt gga gga gag ctg aaa ggg	2352
Glu Ser Gln Thr Gly Glu Pro Gly Trp Leu Gly Gly Glu Leu Lys Gly	
770 775 780	
aag acg gga tgg ttc cct gca aac tat gca gaa aag att cca gaa aat	2400
Lys Thr Gly Trp Phe Pro Ala Asn Tyr Ala Glu Lys Ile Pro Glu Asn	
785 790 795 800	
gag gtt ccc act cca gcc aaa cca gtg acc gat ctg aca tct gcc cct	2448
Glu Val Pro Thr Pro Ala Lys Pro Val Thr Asp Leu Thr Ser Ala Pro	
805 810 815	
gcc ccc aaa ctg gct ctg cgt gag acc cct gct cct ttg cca gtg acc	2496
Ala Pro Lys Leu Ala Leu Arg Glu Thr Pro Ala Pro Leu Pro Val Thr	
820 825 830	
tct tct gag ccc tcc aca acc ccc aac aac tgg gca gac ttc agt tcc	2544
Ser Ser Glu Pro Ser Thr Thr Pro Asn Asn Trp Ala Asp Phe Ser Ser	
835 840 845	
acg tgg ccc agc agc tca aac gag aag cca gaa acg gac aac tgg gat	2592
Thr Trp Pro Ser Ser Ser Asn Glu Lys Pro Glu Thr Asp Asn Trp Asp	
850 855 860	
acg tgg gcg gct cag cct tct ctg acc gta cct agt gct ggc cag tta	2640
Thr Trp Ala Ala Gln Pro Ser Leu Thr Val Pro Ser Ala Gly Gln Leu	
865 870 875 880	
cgg cag aga tca gcc ttt acc cca gcc aca gcc act ggc tcc tcc cca	2688
Arg Gln Arg Ser Ala Phe Thr Pro Ala Thr Ala Thr Gly Ser Ser Pro	
885 890 895	
tct ccc gtc ctg ggc cag ggt gaa aag gtg gaa ggg cta caa gcg caa	2736
Ser Pro Val Leu Gly Gln Gly Glu Lys Val Glu Gly Leu Gln Ala Gln	
900 905 910	
gcc ctg tat ccc tgg aga gcc aaa aaa gac aac cac tta aat ttt aac	2784
Ala Leu Tyr Pro Trp Arg Ala Lys Lys Asp Asn His Leu Asn Phe Asn	
915 920 925	
aaa agt gac gtc atc acc gtt ctg gaa cag caa gac atg tgg tgg ttt	2832
Lys Ser Asp Val Ile Thr Val Leu Glu Gln Gln Asp Met Trp Trp Phe	
930 935 940	
gga gaa gtt caa ggt cag aag ggt tgg ttc ccc aag tct tac gtg aaa	2880

Gly	Glu	Val	Gln	Gly	Gln	Lys	Gly	Trp	Phe	Pro	Lys	Ser	Tyr	Val	Lys	
945					950					955					960	
ctc	att	tca	ggg	ccc	gta	agg	aaa	tcc	aca	agc	atc	gat	act	ggc	cct	2928
Leu	Ile	Ser	Gly	Pro	Val	Arg	Lys	Ser	Thr	Ser	Ile	Asp	Thr	Gly	Pro	
				965					970					975		
act	gaa	agt	cct	gct	agt	cta	aag	aga	gtg	gct	tcc	ccg	gcc	gcc	aag	2976
Thr	Glu	Ser	Pro	Ala	Ser	Leu	Lys	Arg	Val	Ala	Ser	Pro	Ala	Ala	Lys	
				980				985					990			
cca	gcc	att	ccc	gga	gaa	gag	ttt	att	gcc	atg	tac	aca	tac	gag	agt	3024
Pro	Ala	Ile	Pro	Gly	Glu	Glu	Phe	Ile	Ala	Met	Tyr	Thr	Tyr	Glu	Ser	
		995					1000						1005			
tct	gag	caa	gga	gat	tta	acc	ttt	cag	caa	ggg	gat	gtg	att	gtg		3069
Ser	Glu	Gln	Gly	Asp	Leu	Thr	Phe	Gln	Gln	Gly	Asp	Val	Ile	Val		
	1010					1015					1020					
gtt	acc	aag	aaa	gat	ggt	gac	tgg	tgg	acg	gga	acg	gtg	ggc	gac		3114
Val	Thr	Lys	Lys	Asp	Gly	Asp	Trp	Trp	Thr	Gly	Thr	Val	Gly	Asp		
	1025					1030					1035					
aag	tcc	gga	gtc	ttc	cct	tct	aac	tat	gtg	agg	ctt	aaa	gat	tca		3159
Lys	Ser	Gly	Val	Phe	Pro	Ser	Asn	Tyr	Val	Arg	Leu	Lys	Asp	Ser		
	1040					1045					1050					
gag	ggc	tct	gga	act	gct	ggg	aaa	aca	ggg	agt	tta	gga	aaa	aaa		3204
Glu	Gly	Ser	Gly	Thr	Ala	Gly	Lys	Thr	Gly	Ser	Leu	Gly	Lys	Lys		
	1055					1060					1065					
cct	gaa	att	gcc	cag	gtt	att	gct	tcc	tac	gct	gct	act	ggt	ccc		3249
Pro	Glu	Ile	Ala	Gln	Val	Ile	Ala	Ser	Tyr	Ala	Ala	Thr	Gly	Pro		
	1070					1075					1080					
gaa	caa	ctc	acc	ctg	gct	cct	ggg	cag	ctg	att	ctg	atc	cgg	aaa		3294
Glu	Gln	Leu	Thr	Leu	Ala	Pro	Gly	Gln	Leu	Ile	Leu	Ile	Arg	Lys		
	1085					1090					1095					
aag	aac	cca	ggt	gga	tgg	tgg	gaa	gga	gaa	ctg	caa	gct	cga	ggg		3339
Lys	Asn	Pro	Gly	Gly	Trp	Trp	Glu	Gly	Glu	Leu	Gln	Ala	Arg	Gly		
	1100					1105					1110					
aaa	aag	cgc	cag	ata	ggg	tgg	ttt	cca	gca	aat	tat	gtc	aaa	ctt		3384
Lys	Lys	Arg	Gln	Ile	Gly	Trp	Phe	Pro	Ala	Asn	Tyr	Val	Lys	Leu		
	1115					1120					1125					
cta	agc	ccc	gga	aca	agc	aaa	atc	acc	cca	act	gag	cta	ccc	aag		3429
Leu	Ser	Pro	Gly	Thr	Ser	Lys	Ile	Thr	Pro	Thr	Glu	Leu	Pro	Lys		
	1130					1135					1140					
acc	gca	gtg	cag	cca	gca	gtg	tgc	cag	gtg	atc	ggg	atg	tac	gat		3474
Thr	Ala	Val	Gln	Pro	Ala	Val	Cys	Gln	Val	Ile	Gly	Met	Tyr	Asp		
	1145					1150					1155					
tac	acc	gcc	cag	aac	gat	gac	gaa	cta	gcc	ttc	agc	aaa	ggc	cag		3519
Tyr	Thr	Ala	Gln	Asn	Asp	Asp	Glu	Leu	Ala	Phe	Ser	Lys	Gly	Gln		

1160	1165	1170	
atc atc aac gtc ctc aac aag	gag gac ccg gac	tgg tgg aaa gga	3564
Ile Ile Asn Val Leu Asn Lys	Glu Asp Pro Asp	Trp Trp Lys Gly	
1175	1180	1185	
gaa gtc agt ggg caa gtt ggg	ctc ttc cca tcc aat	tat gta aag	3609
Glu Val Ser Gly Gln Val Gly	Leu Phe Pro Ser	Tyr Val Lys	
1190	1195	1200	
ctg acc aca gac atg gac ccc	agc cag caa tgg tgc	tca gac ctg	3654
Leu Thr Thr Asp Met Asp	Pro Ser Gln Gln Trp	Cys Ser Asp Leu	
1205	1210	1215	
cat ctc tta gat atg ctg acc	ccg act gag agg aag	cgg caa ggc	3699
His Leu Leu Asp Met Leu Thr	Pro Thr Glu Arg	Lys Arg Gln Gly	
1220	1225	1230	
tac atc cat gaa ctc att gtc	acg gag gag aac tac	gtg aac gac	3744
Tyr Ile His Glu Leu Ile Val	Thr Glu Glu Asn Tyr	Val Asn Asp	
1235	1240	1245	
ttg cag ctg gtc aca gag atc	ttt cag aaa ccc ctg	acg gag tct	3789
Leu Gln Leu Val Thr Glu Ile	Phe Gln Lys Pro	Leu Thr Glu Ser	
1250	1255	1260	
gag ctg ctg aca gaa aaa gag	gtt gct atg att ttt	gtt aac tgg	3834
Glu Leu Leu Thr Glu Lys Glu	Val Ala Met Ile Phe	Val Asn Trp	
1265	1270	1275	
aag gag ctg atc atg tgt aat	atc aaa ctg ctg aaa	gcg ctg aga	3879
Lys Glu Leu Ile Met Cys Asn	Ile Lys Leu Leu Lys	Ala Leu Arg	
1280	1285	1290	
gtc cgc aag aag atg tct ggg	gag aag atg ccg gtg	aag atg att	3924
Val Arg Lys Lys Met Ser Gly	Glu Lys Met Pro	Val Lys Met Ile	
1295	1300	1305	
ggc gac atc ctg agc gcc cag	ctg ccg cac atg cag	cct tac atc	3969
Gly Asp Ile Leu Ser Ala Gln	Leu Pro His Met	Gln Pro Tyr Ile	
1310	1315	1320	
cgc ttc tgc agc tgc cag ctc	aat ggg gct gcc ctc	atc cag cag	4014
Arg Phe Cys Ser Cys Gln Leu	Asn Gly Ala Ala Leu	Ile Gln Gln	
1325	1330	1335	
aag acg gac gag gct cca gac	ttc aag gag ttc gtc	aaa aga ctg	4059
Lys Thr Asp Glu Ala Pro Asp	Phe Lys Glu Phe Val	Lys Arg Leu	
1340	1345	1350	
gca atg gac cct ccg tgc aaa	gga atg cct ctg tcc	agc ttt ata	4104
Ala Met Asp Pro Arg Cys Lys	Gly Met Pro Leu Ser	Ser Phe Ile	
1355	1360	1365	
ctg aag cct atg cag cgt gtc	aca aga tac ccg ctg	atc att aaa	4149
Leu Lys Pro Met Gln Arg Val	Thr Arg Tyr Pro	Ile Ile Lys	
1370	1375	1380	

aac atc ctg gaa aac act cct gag aac cat cca gac cac agc cac	4194
Asn Ile Leu Glu Asn Thr Pro Glu Asn His Pro Asp His Ser His	
1385 1390 1395	
ctg aag cat gcc ctg gaa aag gcg gag gag ctg tgc tcc cag gtg	4239
Leu Lys His Ala Leu Glu Lys Ala Glu Glu Leu Cys Ser Gln Val	
1400 1405 1410	
aac gag gga gtt cga gag aag gag aac tca gac cgg ctg gag tgg	4284
Asn Glu Gly Val Arg Glu Lys Glu Asn Ser Asp Arg Leu Glu Trp	
1415 1420 1425	
atc caa gcc cac gtg cag tgt gaa ggc ctt tct gag caa ctg gtg	4329
Ile Gln Ala His Val Gln Cys Glu Gly Leu Ser Glu Gln Leu Val	
1430 1435 1440	
ttc aat tca gtg acc aac tgc ttg gga cca cgc aag ttt ctg cac	4374
Phe Asn Ser Val Thr Asn Cys Leu Gly Pro Arg Lys Phe Leu His	
1445 1450 1455	
agc ggg aag ctc tac aag gcc aag agc aat aaa gaa ctg tat ggc	4419
Ser Gly Lys Leu Tyr Lys Ala Lys Ser Asn Lys Glu Leu Tyr Gly	
1460 1465 1470	
ttc ctc ttc aac gac ttc ctc ctg ctg acc caa atc aca aag ccc	4464
Phe Leu Phe Asn Asp Phe Leu Leu Leu Thr Gln Ile Thr Lys Pro	
1475 1480 1485	
tta ggc tct tcc ggc acc gac aaa gtc ttc agc ccc aaa tct aac	4509
Leu Gly Ser Ser Gly Thr Asp Lys Val Phe Ser Pro Lys Ser Asn	
1490 1495 1500	
ctt cag tat aaa atg tac aaa acg ccc att ttc tta aat gag gtt	4554
Leu Gln Tyr Lys Met Tyr Lys Thr Pro Ile Phe Leu Asn Glu Val	
1505 1510 1515	
cta gta aaa ttg ccc acg gac cct tct gga gat gag cct atc ttc	4599
Leu Val Lys Leu Pro Thr Asp Pro Ser Gly Asp Glu Pro Ile Phe	
1520 1525 1530	
cac att tcc cac atc gac cgg gtc tac acc ctc cga gca gag agc	4644
His Ile Ser His Ile Asp Arg Val Tyr Thr Leu Arg Ala Glu Ser	
1535 1540 1545	
ata aat gag agg act gcc tgg gtg cag aaa atc aag gcg gcg tct	4689
Ile Asn Glu Arg Thr Ala Trp Val Gln Lys Ile Lys Ala Ala Ser	
1550 1555 1560	
gag ctc tac ata gag acg gag aaa aag aag cga gag aag gcg tac	4734
Glu Leu Tyr Ile Glu Thr Glu Lys Lys Lys Arg Glu Lys Ala Tyr	
1565 1570 1575	
ctg gtc cgt tcc cag cgg gcg acc ggt att gga agg ttg atg gtg	4779
Leu Val Arg Ser Gln Arg Ala Thr Gly Ile Gly Arg Leu Met Val	
1580 1585 1590	

aac gtg gta gaa ggc att gag ctg aag ccc tgt cgg tca cat gga	4824
Asn Val Val Glu Gly Ile Glu Leu Lys Pro Cys Arg Ser His Gly	
1595 1600 1605	
aag agc aac ccg tac tgt gag gtg acc atg ggc tct cag tgc cac	4869
Lys Ser Asn Pro Tyr Cys Glu Val Thr Met Gly Ser Gln Cys His	
1610 1615 1620	
atc acc aag aca atc cag gac acg cta aac ccc aag tgg aat tct	4914
Ile Thr Lys Thr Ile Gln Asp Thr Leu Asn Pro Lys Trp Asn Ser	
1625 1630 1635	
aac tgc cag ttc ttc atc aga gac ctg gag cag gag gtt ctc tgc	4959
Asn Cys Gln Phe Phe Ile Arg Asp Leu Glu Gln Glu Val Leu Cys	
1640 1645 1650	
atc aca gtg ttt gag agg gac cag ttc tcg cct gat gat ttt ttg	5004
Ile Thr Val Phe Glu Arg Asp Gln Phe Ser Pro Asp Asp Phe Leu	
1655 1660 1665	
ggc cgg aca gag atc cga gtg gcc gac atc aag aaa gac cag ggc	5049
Gly Arg Thr Glu Ile Arg Val Ala Asp Ile Lys Lys Asp Gln Gly	
1670 1675 1680	
tcc aag ggg ccg gtt acg aag tgt ctc ctg ctg cat gag gtc ccc	5094
Ser Lys Gly Pro Val Thr Lys Cys Leu Leu Leu His Glu Val Pro	
1685 1690 1695	
acg gga gag att gtg gtc cgc ctt gac ctg cag ttg ttt gat gag	5139
Thr Gly Glu Ile Val Val Arg Leu Asp Leu Gln Leu Phe Asp Glu	
1700 1705 1710	
ccg tag	5145
Pro	

<210> 24  
 <211> 1714  
 <212> PRT  
 <213> Mus musculus

<400> 24

Met Ala Gln Phe Pro Thr Pro Phe Gly Gly Ser Leu Asp Val Trp Ala
1 5 10 15

Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe Leu Ser Leu
20 25 30

Lys Pro Ile Ala Gly Phe Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe
35 40 45

Phe Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu

50	55	60
Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Val Glu Phe Ser Ile 65 70 75 80		
Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Tyr Gln Leu Pro Ser 85 90 95		
Thr Leu Pro Pro Val Met Lys Gln Gln Pro Val Ala Ile Ser Ser Ala 100 105 110		
Pro Ala Phe Gly Ile Gly Gly Ile Ala Ser Met Pro Pro Leu Thr Ala 115 120 125		
Val Ala Pro Val Pro Met Gly Ser Ile Pro Val Val Gly Met Ser Pro 130 135 140		
Pro Leu Val Ser Ser Val Pro Pro Ala Ala Val Pro Pro Leu Ala Asn 145 150 155 160		
Gly Ala Pro Pro Val Ile Gln Pro Leu Pro Ala Phe Ala His Pro Ala 165 170 175		
Ala Thr Trp Pro Lys Ser Ser Ser Phe Ser Arg Ser Gly Pro Gly Ser 180 185 190		
Gln Leu Asn Thr Lys Leu Gln Lys Ala Gln Ser Phe Asp Val Ala Ser 195 200 205		
Ala Pro Pro Ala Ala Glu Trp Ala Val Pro Gln Ser Ser Arg Leu Lys 210 215 220		
Tyr Arg Gln Leu Phe Asn Ser His Asp Lys Thr Met Ser Gly His Leu 225 230 235 240		
Thr Gly Pro Gln Ala Arg Thr Ile Leu Met Gln Ser Ser Leu Pro Gln 245 250 255		
Ala Gln Leu Ala Ser Ile Trp Asn Leu Ser Asp Ile Asp Gln Asp Gly 260 265 270		
Lys Leu Thr Ala Glu Glu Phe Ile Leu Ala Met His Leu Ile Asp Val 275 280 285		

Ala Met Ser Gly Gln Pro Leu Pro Pro Val Leu Pro Pro Glu Tyr Ile  
 290 295 300

Pro Pro Ser Phe Arg Arg Val Arg Ser Gly Ser Gly Met Ser Val Ile  
 305 310 315 320

Ser Ser Ser Ser Val Asp Gln Arg Leu Pro Glu Glu Pro Ser Ser Glu  
 325 330 335

Asp Glu Gln Gln Pro Glu Lys Lys Leu Pro Val Thr Phe Glu Asp Lys  
 340 345 350

Lys Arg Glu Asn Phe Glu Arg Gly Ser Val Glu Leu Glu Lys Arg Arg  
 355 360 365

Gln Ala Leu Leu Glu Gln Gln Arg Lys Glu Gln Glu Arg Leu Ala Gln  
 370 375 380

Leu Glu Arg Ala Glu Gln Glu Arg Lys Glu Arg Glu Arg Gln Glu Gln  
 385 390 395 400

Glu Ala Lys Arg Gln Leu Glu Leu Glu Lys Gln Leu Glu Lys Gln Arg  
 405 410 415

Glu Leu Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg  
 420 425 430

Arg Glu Ala Ala Lys Arg Glu Leu Glu Arg Gln Arg Gln Leu Glu Trp  
 435 440 445

Glu Arg Asn Arg Arg Gln Glu Leu Leu Asn Gln Arg Asn Lys Glu Gln  
 450 455 460

Glu Gly Thr Val Val Leu Lys Ala Arg Arg Lys Thr Leu Glu Phe Glu  
 465 470 475 480

Leu Glu Ala Leu Asn Asp Lys Lys His Gln Leu Glu Gly Lys Leu Gln  
 485 490 495

Asp Ile Arg Cys Arg Leu Ala Thr Gln Arg Gln Glu Ile Glu Ser Thr  
 500 505 510

Asn Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln Gln  
515 520 525

Gln Leu Gln Glu Ser Gln Gln Met Leu Gly Arg Leu Ile Pro Glu Lys  
530 535 540

Gln Ile Leu Ser Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu His  
545 550 555 560

Arg Asp Ser Leu Leu Thr Leu Lys Arg Ala Leu Glu Ala Lys Glu Leu  
565 570 575

Ala Arg Gln Gln Leu Arg Glu Gln Leu Asp Glu Val Glu Arg Glu Thr  
580 585 590

Arg Ser Lys Leu Gln Glu Ile Asp Val Phe Asn Asn Gln Leu Lys Glu  
595 600 605

Leu Arg Glu Ile His Ser Lys Gln Gln Leu Gln Lys Gln Arg Ser Leu  
610 615 620

Glu Ala Ala Arg Leu Lys Gln Lys Glu Gln Glu Arg Lys Ser Leu Glu  
625 630 635 640

Leu Glu Lys Gln Lys Glu Asp Ala Gln Arg Arg Val Gln Glu Arg Asp  
645 650 655

Lys Gln Trp Leu Glu His Val Gln Gln Glu Glu Gln Pro Arg Pro Arg  
660 665 670

Lys Pro His Glu Glu Asp Arg Leu Lys Arg Glu Asp Ser Val Arg Lys  
675 680 685

Lys Glu Ala Glu Glu Arg Ala Lys Pro Glu Met Gln Asp Lys Gln Ser  
690 695 700

Arg Leu Phe His Pro His Gln Glu Pro Ala Lys Leu Ala Thr Gln Ala  
705 710 715 720

Pro Trp Ser Thr Thr Glu Lys Gly Pro Leu Thr Ile Ser Ala Gln Glu  
725 730 735



Ser Val Lys Val Val Tyr Tyr Arg Ala Leu Tyr Pro Phe Glu Ser Arg  
740 745 750

Ser His Asp Glu Ile Thr Ile Gln Pro Gly Asp Ile Val Met Val Asp  
755 760 765

Glu Ser Gln Thr Gly Glu Pro Gly Trp Leu Gly Gly Glu Leu Lys Gly  
770 775 780

Lys Thr Gly Trp Phe Pro Ala Asn Tyr Ala Glu Lys Ile Pro Glu Asn  
785 790 795 800

Glu Val Pro Thr Pro Ala Lys Pro Val Thr Asp Leu Thr Ser Ala Pro  
805 810 815

Ala Pro Lys Leu Ala Leu Arg Glu Thr Pro Ala Pro Leu Pro Val Thr  
820 825 830

Ser Ser Glu Pro Ser Thr Thr Pro Asn Asn Trp Ala Asp Phe Ser Ser  
835 840 845

Thr Trp Pro Ser Ser Ser Asn Glu Lys Pro Glu Thr Asp Asn Trp Asp  
850 855 860

Thr Trp Ala Ala Gln Pro Ser Leu Thr Val Pro Ser Ala Gly Gln Leu  
865 870 875 880

Arg Gln Arg Ser Ala Phe Thr Pro Ala Thr Ala Thr Gly Ser Ser Pro  
885 890 895

Ser Pro Val Leu Gly Gln Gly Glu Lys Val Glu Gly Leu Gln Ala Gln  
900 905 910

Ala Leu Tyr Pro Trp Arg Ala Lys Lys Asp Asn His Leu Asn Phe Asn  
915 920 925

Lys Ser Asp Val Ile Thr Val Leu Glu Gln Gln Asp Met Trp Trp Phe  
930 935 940

Gly Glu Val Gln Gly Gln Lys Gly Trp Phe Pro Lys Ser Tyr Val Lys  
945 950 955 960

Leu Ile Ser Gly Pro Val Arg Lys Ser Thr Ser Ile Asp Thr Gly Pro

	965		970		975
Thr Glu Ser	Pro Ala Ser Leu Lys Arg Val Ala Ser Pro Ala Ala Lys				
	980		985		990
Pro Ala Ile	Pro Gly Glu Glu Phe Ile Ala Met Tyr Thr Tyr Glu Ser				
	995		1000		1005
Ser Glu Gln Gly Asp Leu Thr Phe Gln Gln Gly Asp Val Ile Val					
1010		1015		1020	
Val Thr Lys Lys Asp Gly Asp Trp Trp Thr Gly Thr Val Gly Asp					
1025		1030		1035	
Lys Ser Gly Val Phe Pro Ser Asn Tyr Val Arg Leu Lys Asp Ser					
1040		1045		1050	
Glu Gly Ser Gly Thr Ala Gly Lys Thr Gly Ser Leu Gly Lys Lys					
1055		1060		1065	
Pro Glu Ile Ala Gln Val Ile Ala Ser Tyr Ala Ala Thr Gly Pro					
1070		1075		1080	
Glu Gln Leu Thr Leu Ala Pro Gly Gln Leu Ile Leu Ile Arg Lys					
1085		1090		1095	
Lys Asn Pro Gly Gly Trp Trp Glu Gly Glu Leu Gln Ala Arg Gly					
1100		1105		1110	
Lys Lys Arg Gln Ile Gly Trp Phe Pro Ala Asn Tyr Val Lys Leu					
1115		1120		1125	
Leu Ser Pro Gly Thr Ser Lys Ile Thr Pro Thr Glu Leu Pro Lys					
1130		1135		1140	
Thr Ala Val Gln Pro Ala Val Cys Gln Val Ile Gly Met Tyr Asp					
1145		1150		1155	
Tyr Thr Ala Gln Asn Asp Asp Glu Leu Ala Phe Ser Lys Gly Gln					
1160		1165		1170	
Ile Ile Asn Val Leu Asn Lys Glu Asp Pro Asp Trp Trp Lys Gly					
1175		1180		1185	

Glu Val Ser Gly Gln Val Gly Leu Phe Pro Ser Asn Tyr Val Lys		
1190	1195	1200
Leu Thr Thr Asp Met Asp Pro Ser Gln Gln Trp Cys Ser Asp Leu		
1205	1210	1215
His Leu Leu Asp Met Leu Thr Pro Thr Glu Arg Lys Arg Gln Gly		
1220	1225	1230
Tyr Ile His Glu Leu Ile Val Thr Glu Glu Asn Tyr Val Asn Asp		
1235	1240	1245
Leu Gln Leu Val Thr Glu Ile Phe Gln Lys Pro Leu Thr Glu Ser		
1250	1255	1260
Glu Leu Leu Thr Glu Lys Glu Val Ala Met Ile Phe Val Asn Trp		
1265	1270	1275
Lys Glu Leu Ile Met Cys Asn Ile Lys Leu Leu Lys Ala Leu Arg		
1280	1285	1290
Val Arg Lys Lys Met Ser Gly Glu Lys Met Pro Val Lys Met Ile		
1295	1300	1305
Gly Asp Ile Leu Ser Ala Gln Leu Pro His Met Gln Pro Tyr Ile		
1310	1315	1320
Arg Phe Cys Ser Cys Gln Leu Asn Gly Ala Ala Leu Ile Gln Gln		
1325	1330	1335
Lys Thr Asp Glu Ala Pro Asp Phe Lys Glu Phe Val Lys Arg Leu		
1340	1345	1350
Ala Met Asp Pro Arg Cys Lys Gly Met Pro Leu Ser Ser Phe Ile		
1355	1360	1365
Leu Lys Pro Met Gln Arg Val Thr Arg Tyr Pro Leu Ile Ile Lys		
1370	1375	1380
Asn Ile Leu Glu Asn Thr Pro Glu Asn His Pro Asp His Ser His		
1385	1390	1395

Leu Lys	His Ala	Leu Glu	Lys	Ala Glu	Glu Leu	Cys	Ser Gln	Val
1400			1405			1410		
Asn Glu	Gly Val	Arg Glu	Lys	Glu Asn	Ser Asp	Arg	Leu Glu	Trp
1415			1420			1425		
Ile Gln	Ala His	Val Gln	Cys	Glu Gly	Leu Ser	Glu	Gln Leu	Val
1430			1435			1440		
Phe Asn	Ser Val	Thr Asn	Cys	Leu Gly	Pro Arg	Lys	Phe Leu	His
1445			1450			1455		
Ser Gly	Lys Leu	Tyr Lys	Ala	Lys Ser	Asn Lys	Glu	Leu Tyr	Gly
1460			1465			1470		
Phe Leu	Phe Asn	Asp Phe	Leu	Leu Leu	Thr Gln	Ile	Thr Lys	Pro
1475			1480			1485		
Leu Gly	Ser Ser	Gly Thr	Asp	Lys Val	Phe Ser	Pro	Lys Ser	Asn
1490			1495			1500		
Leu Gln	Tyr Lys	Met Tyr	Lys	Thr Pro	Ile Phe	Leu	Asn Glu	Val
1505			1510			1515		
Leu Val	Lys Leu	Pro Thr	Asp	Pro Ser	Gly Asp	Glu	Pro Ile	Phe
1520			1525			1530		
His Ile	Ser His	Ile Asp	Arg	Val Tyr	Thr Leu	Arg	Ala Glu	Ser
1535			1540			1545		
Ile Asn	Glu Arg	Thr Ala	Trp	Val Gln	Lys Ile	Lys	Ala Ala	Ser
1550			1555			1560		
Glu Leu	Tyr Ile	Glu Thr	Glu	Lys Lys	Lys Arg	Glu	Lys Ala	Tyr
1565			1570			1575		
Leu Val	Arg Ser	Gln Arg	Ala	Thr Gly	Ile Gly	Arg	Leu Met	Val
1580			1585			1590		
Asn Val	Val Glu	Gly Ile	Glu	Leu Lys	Pro Cys	Arg	Ser His	Gly
1595			1600			1605		

Lys Ser Asn Pro Tyr Cys Glu Val Thr Met Gly Ser Gln Cys His  
 1610 1615 1620

Ile Thr Lys Thr Ile Gln Asp Thr Leu Asn Pro Lys Trp Asn Ser  
 1625 1630 1635

Asn Cys Gln Phe Phe Ile Arg Asp Leu Glu Gln Glu Val Leu Cys  
 1640 1645 1650

Ile Thr Val Phe Glu Arg Asp Gln Phe Ser Pro Asp Asp Phe Leu  
 1655 1660 1665

Gly Arg Thr Glu Ile Arg Val Ala Asp Ile Lys Lys Asp Gln Gly  
 1670 1675 1680

Ser Lys Gly Pro Val Thr Lys Cys Leu Leu Leu His Glu Val Pro  
 1685 1690 1695

Thr Gly Glu Ile Val Val Arg Leu Asp Leu Gln Leu Phe Asp Glu  
 1700 1705 1710

Pro

<210> 25  
 <211> 6014  
 <212> DNA  
 <213> Mus musculus

<400> 25  
 cccttccttt cctttttttg tgttcgctt cggccgtgcc ggctgagagc ccagcagccg 60  
 tgacaggctg cgcaacaggt tcgctgcggc cggcctgacg actgacccgg cggcggcggc 120  
 cgcggcacgg cagggctctt ccggagcttg gccgcgcca cgcgccggtg tcgaggagcg 180  
 cgcggggtcg cgccgggacg tgcgcgaggc gccagatggc tgagagctgc aagaagaagt 240  
 caggatcatg atggctcagt ttcccacagc gatgaatgga gggccaaata tgtgggctat 300  
 tacatctgaa gaacgtacta agcatgataa acagtttgat aacctcaaac cttcaggagg 360  
 ttacataaca ggtgatcaag cccgtacttt tttcctacag tcaggtctgc cggccccggt 420  
 tttagctgaa atatgggcct tatcagatct gaacaaggat gggaagatgg accagcaaga 480  
 gttctctata gctatgaaac tcatcaagtt aaagttgcag ggccaacagc tgcctgtagt 540  
 cctccctcct atcatgaaac aacccctat gttctctcca ctaatctctg ctcgttttgg 600

gatgggaagc atgccaatc tgtccattca tcagccattg cctccagttg cacctatagc	660
aacacccttg tcttctgcta cgtcagggac cagtattcct cccctaata ga tgctgctcc	720
cctagtgcct tctgttagta catcctcatt accaaatgga actgccagtc tcattcagcc	780
tttatccatt ccttattctt cttcaacatt gcctcatgca tcattcttaca gcctgatgat	840
gggaggattt ggtggtgcta gtatccagaa ggcccagtct ctgattgatt taggatctag	900
tagctcaact tcctcaactg cttccctctc agggaaactca cctaagacag ggacctcaga	960
gtgggcagtt cctcagcctt caagattaaa gtatcggcaa aaatttaata gtctagacaa	1020
aggcatgagc ggatacctct caggttttca agctagaaaat gcccttcttc agtcaaatct	1080
ctctcaaact cagctagcta ctatttggac tctggctgac atcgatggtg acggacagtt	1140
gaaagctgaa gaatttattc tggcgatgca cctcactgac atggccaaag ctggacagcc	1200
actaccactg acgttgcttc ccgagcttgt cctccatct ttcagagggg gaaagcaagt	1260
tgattctgtt aatggaactc tgccttcata tcagaaaaca caagaagaag agcctcagaa	1320
gaaactgcc a gttacttttg aggacaaacg gaaagccaac tatgaacgag gaaacatgga	1380
gctggagaag cgacgccaag tgttgatgga gcagcagcag agggaggctg aacgcaaagc	1440
ccagaaagag aaggaagagt gggagcggaa acagagagaa ctgcaagagc aagaatggaa	1500
gaagcagctg gagttggaga aacgcttgga gaaacagaga gagctggaga gacagcggga	1560
ggaagagagg agaaaggaga tagaaagacg agaggcagca aaacaggagc ttgagagaca	1620
acgccgttta gaatgggaaa gactccgtcg gcaggagctg ctcagtcaga agaccaggga	1680
acaagaagac attgtcaggc tgagctccag aaagaaaagt ctccacctgg aactggaagc	1740
agtgaatgga aaacatcagc agatctcagg cagactacaa gatgtccaaa tcagaaagca	1800
aacacaaaag actgagctag aagttttgga taaacagtgt gacctggaaa ttatggaaat	1860
caaacaactt caacaagagc ttaaggaata tcaaaataag cttatctatc tggtccttga	1920
gaagcagcta ttaaacgaaa gaattaaaaa catgcagctc agtaacacac ctgattcagg	1980
gatcagttta cttcataaaa agtcatcaga aaaggaagaa ttatgccaaa gacttaaaga	2040
acaattagat gctcttgaaa aagaaactgc atctaagctc tcagaaatgg attcatttaa	2100
caatcagctg aaggaactca gagaaagcta taatacacag cagttagccc ttgaacaact	2160
tcataaaatc aaacgtgaca aattgaagga aatcgaaaga aaaagattag agcaaatca	2220
aaaaaagaaa ctagaagatg aggctgcaag gaaagcaaag caaggaaaag aaaacttgtg	2280

gagagaaagt	attagaaagg	aagaagagga	aaagcaaaaa	cgactccagg	aagaaaagtc	2340
acaggacaaa	actcaagaag	aggaacgaaa	agctgaggca	aaacaaagt	agacagccag	2400
tgctttggtg	aattacagag	cactgtaccc	ttttgaagca	agaaaccatg	atgagatgag	2460
ttttagttct	ggggatataa	ttcaggttga	tgaaaaaact	gtaggagagc	ctggttggct	2520
ttatggtagt	tttcagggaa	agtttggctg	gttcccctgc	aactatgtag	aaaaagtgc	2580
gtcaagtga	aaagctctgt	ctcctaagaa	ggccttactt	cctcctacag	tgtctctctc	2640
tgctacctca	acttcttccc	agccaccagc	atcagtgact	gattatcaca	atgtatcctt	2700
ctcaaaccct	actgttaata	caacatggca	gcagaagtca	gctttttacc	gcactgtgtc	2760
ccttgatct	gtgtccccc	ttcacggaca	ggggcaggct	gtagaaaacc	tgaaagccca	2820
ggccctttgt	tcctggacgg	caaagaagga	gaaccacctg	aacttctcaa	agcacgacgt	2880
catcactgtc	ctggagcagc	aggaaaactg	gtggtttggg	gaggtgcacg	gaggaagagg	2940
atggttcccc	aagtcttatg	tcaagctcat	tcctgggaat	gaagtacagc	gaggagagcc	3000
agaagctttg	tatgcagctg	tgactaagaa	acctacctcc	acagcctatc	cagttacctc	3060
cacagcctat	ccagttggag	aagactacat	tgcactttat	tcataactca	gtgtagagcc	3120
cggggatttg	actttcactg	aaggtgaaga	aattctagt	accagaaaag	atggagagt	3180
gtggacagga	agtattggag	agagaactgg	aatcttcccg	tccaactacg	tcagaccaaa	3240
ggatcaagag	aattttggga	atgctagcaa	atctggagca	tcaaacaaaa	aacccgagat	3300
cgctcaagta	acttcagcat	atgctgcttc	agggactgag	cagctcagcc	ttgcgccagg	3360
acagttaata	ttaatcttaa	agaaaaacac	aagcgggtgg	tggcaaggag	agctacaggc	3420
cagaggggaag	aaacgacaga	agggatgggt	tcctgccagc	catgtaaagc	tgctaggtcc	3480
aagcagtga	agaaccatgc	ctacttttca	cgctgtatgt	caagtgattg	ctatgtatga	3540
ctacatggcg	aataacgaag	atgagctcaa	tttctccaaa	ggacagctga	ttaatgttat	3600
gaacaaagat	gaccctgact	ggtggcaagg	agaaaccaat	ggtctgactg	gtctctttcc	3660
ttcaaactat	gttaagatga	caacagactc	agatccaagt	caacagtggg	gtgctgacct	3720
ccaagccctg	gacacaatgc	agcctacgga	gaggaagcga	cagggctaca	ttcacgagct	3780
cattcagaca	gaggagcggg	acatggacga	cgacctgcag	ctggctcatg	aggtcttcca	3840
gaaacggatg	gctgaggaag	gcttcctcac	tgaagcagac	atggctctga	tctttgtgaa	3900
ctggaaagag	ctcatcatgt	ccaacacgaa	gctgctgagg	gccttgcggg	tgaggaagaa	3960
gactgggggt	gagaagatgc	cagttcagat	gattggagac	atcctggcgg	cagagctgtc	4020

ccacatgcag gcctacatcc gcttctgcag ctgtcagctt aatggggcaa ccctgttaca	4080
gcagaagaca gacgaggaca cggacttcaa ggaatttcta aagaagttgg catcagaccc	4140
acgatgcaaa gggatgcccc tctccagctt cctgctgaag cccatgcaga ggatcactcg	4200
ctacccgctg ctcatccgaa gtatcctgga gaacactcca cagagtcatg ttgaccactc	4260
ctccctgaag ctggccctag aacgtgctga ggagctgtgc tctcaggtga acgagggagt	4320
ccgggagaag gaaaattcag accggctgga gtggatccag gcacacgtgc agtgcaagg	4380
cttggcagag caacttattt tcaactccct caccaactgc ctgggcccc ggaagcttct	4440
gcacagcggg aagctgtaca agaccaagag caataaggag ctgcacgcct tcctcttcaa	4500
cgacttcctg ctgctcacct acctggtcag gcagtttgcc gccgcctctg gccacgagaa	4560
gctcttcaac tccaagtcca gtgctcagtt ccggatgtac aaaacgcca ttttctgaa	4620
tgaagtgttg gtgaaacttc ccacagaccc ttccggcgat gagcccgctt tccacatttc	4680
ccacattgat cgtgtgtaca cactccgaac agacaacatc aacgagagga cggcctgggt	4740
ccagaagatc aagggtgctt cagagcagta catcgacact gagaagaaga aacgggaaaa	4800
ggcttaccaa gcccgttctc aaaagacttc aggtattggg cgtctgatgg tgcattcat	4860
tgaagctaca gaattaaaag cctgcaaacc aaacgggaaa agtaatccat actgtgaagt	4920
cagcatgggc tcccaaagct ataccaccag gaccctgcag gacacactaa accccaagtg	4980
gaacttcaac tgccagttct tcatcaagga tctttaccag gacgttctgt gtctcactat	5040
gtttgacaga gaccagtttt ctccagatga cttcttgggt cgtactgaag ttccagtggc	5100
aaaaatccga acagaacagg aaagcaaagg cccaccacc cgccgactac tactgcacga	5160
agtccccact ggagaagtct gggtcgctt tgacctgcaa ctttttgaac aaaaaactct	5220
cctttgaggg cctggggaag ccagaaccag gggagctgcc cacaaggctg ggtctaaaga	5280
cagattttgc tctcccagga cagaggagca tcacatggct tcatccatca aacagccaca	5340
ctcgctgggc ctgtatttta ttgcacacta aattgctagc aatctatgca aacatgatct	5400
tttaaacaaa cgccacagca cagtgccttg tactagtgtt aacctgttca gctgtgttag	5460
atgccagggg ttccattttc agggctataa aagtattatg tggaaatgag gcatcagacc	5520
accggacgtt accacttggc aaatctgtcc actgtggagt tggatgatgtt ggaaccattc	5580
cacactatgt gacctctgct gggtcacaca ctccaggagt gaagggctga gatgaaatgc	5640
tgcagccttg gggcttgtgc agcctgatac tgaaatagca tccacttgtg cactgaataa	5700



atagaaactt gatcgtttta ttctgactag atattatcat tctctgctaa gacaatatag 5760  
 tttgaaatat tatagtttga atataaggag gaaagcttga tgtactttta atatactgtg 5820  
 aactctaata atgtggggat atttttcaac tttaattttc ttaagtataa attatttatg 5880  
 taaattcttt gttttgcata tttcatagaa catgcatcct taagctttat cattgccaac 5940  
 aatgtacaga aagagaataa aagtataagt ttatgaatgt aaaaaaaaaa aaaaaaaaaa 6000  
 aaaaaaaaaa aaaa 6014

<210> 26  
 <211> 4977  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)..(4977)  
 <223> Mouse Ese2L

<400> 26  
 atg gct cag ttt ccc aca gcg atg aat gga ggg cca aat atg tgg gct 48  
 Met Ala Gln Phe Pro Thr Ala Met Asn Gly Gly Pro Asn Met Trp Ala  
 1 5 10 15  
 att aca tct gaa gaa cgt act aag cat gat aaa cag ttt gat aac ctc 96  
 Ile Thr Ser Glu Glu Arg Thr Lys His Asp Lys Gln Phe Asp Asn Leu  
 20 25 30  
 aaa cct tca gga ggt tac ata aca ggt gat caa gcc cgt act ttt ttc 144  
 Lys Pro Ser Gly Gly Tyr Ile Thr Gly Asp Gln Ala Arg Thr Phe Phe  
 35 40 45  
 cta cag tca ggt ctg ccg gcc ccg gtt tta gct gaa ata tgg gcc tta 192  
 Leu Gln Ser Gly Leu Pro Ala Pro Val Leu Ala Glu Ile Trp Ala Leu  
 50 55 60  
 tca gat ctg aac aag gat ggg aag atg gac cag caa gag ttc tct ata 240  
 Ser Asp Leu Asn Lys Asp Gly Lys Met Asp Gln Gln Glu Phe Ser Ile  
 65 70 75 80  
 gct atg aaa ctc atc aag tta aag ttg cag ggc caa cag ctg cct gta 288  
 Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Gln Gln Leu Pro Val  
 85 90 95  
 gtc ctc cct cct atc atg aaa caa ccc cct atg ttc tct cca cta atc 336  
 Val Leu Pro Pro Ile Met Lys Gln Pro Pro Met Phe Ser Pro Leu Ile  
 100 105 110  
 tct gct cgt ttt ggg atg gga agc atg ccc aat ctg tcc att cat cag 384  
 Ser Ala Arg Phe Gly Met Gly Ser Met Pro Asn Leu Ser Ile His Gln  
 115 120 125

cca ttg cct cca gtt gca cct ata gca aca ccc ttg tct tct gct acg	432
Pro Leu Pro Pro Val Ala Pro Ile Ala Thr Pro Leu Ser Ser Ala Thr	
130 135 140	
tca ggg acc agt att cct ccc cta atg atg cct gct ccc cta gtg cct	480
Ser Gly Thr Ser Ile Pro Pro Leu Met Met Pro Ala Pro Leu Val Pro	
145 150 155 160	
tct gtt agt aca tcc tca tta cca aat gga act gcc agt ctc att cag	528
Ser Val Ser Thr Ser Ser Leu Pro Asn Gly Thr Ala Ser Leu Ile Gln	
165 170 175	
cct tta tcc att cct tat tct tct tca aca ttg cct cat gca tca tct	576
Pro Leu Ser Ile Pro Tyr Ser Ser Ser Thr Leu Pro His Ala Ser Ser	
180 185 190	
tac agc ctg atg atg gga gga ttt ggt ggt gct agt atc cag aag gcc	624
Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala	
195 200 205	
cag tct ctg att gat tta gga tct agt agc tca act tcc tca act gct	672
Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Ser Thr Ser Ser Thr Ala	
210 215 220	
tcc ctc tca ggg aac tca cct aag aca ggg acc tca gag tgg gca gtt	720
Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val	
225 230 235 240	
cct cag cct tca aga tta aag tat cgg caa aaa ttt aat agt cta gac	768
Pro Gln Pro Ser Arg Leu Lys Tyr Arg Gln Lys Phe Asn Ser Leu Asp	
245 250 255	
aaa ggc atg agc gga tac ctc tca ggt ttt caa gct aga aat gcc ctt	816
Lys Gly Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu	
260 265 270	
ctt cag tca aat ctc tct caa act cag cta gct act att tgg act ctg	864
Leu Gln Ser Asn Leu Ser Gln Thr Gln Leu Ala Thr Ile Trp Thr Leu	
275 280 285	
gct gac atc gat ggt gac gga cag ttg aaa gct gaa gaa ttt att ctg	912
Ala Asp Ile Asp Gly Asp Gly Gln Leu Lys Ala Glu Glu Phe Ile Leu	
290 295 300	
gcg atg cac ctc act gac atg gcc aaa gct gga cag cca cta cca ctg	960
Ala Met His Leu Thr Asp Met Ala Lys Ala Gly Gln Pro Leu Pro Leu	
305 310 315 320	
acg ttg cct ccc gag ctt gtc cct cca tct ttc aga ggg gga aag caa	1008
Thr Leu Pro Pro Glu Leu Val Pro Pro Ser Phe Arg Gly Gly Lys Gln	
325 330 335	
gtt gat tct gtt aat gga act ctg cct tca tat cag aaa aca caa gaa	1056
Val Asp Ser Val Asn Gly Thr Leu Pro Ser Tyr Gln Lys Thr Gln Glu	
340 345 350	
gaa gag cct cag aag aaa ctg cca gtt act ttt gag gac aaa cgg aaa	1104

Glu	Glu	Pro	Gln	Lys	Lys	Leu	Pro	Val	Thr	Phe	Glu	Asp	Lys	Arg	Lys		
		355					360					365					
gcc	aac	tat	gaa	cga	gga	aac	atg	gag	ctg	gag	aag	cga	cgc	caa	gtg		1152
Ala	Asn	Tyr	Glu	Arg	Gly	Asn	Met	Glu	Leu	Glu	Lys	Arg	Arg	Gln	Val		
	370					375					380						
ttg	atg	gag	cag	cag	cag	agg	gag	gct	gaa	cgc	aaa	gcc	cag	aaa	gag		1200
Leu	Met	Glu	Gln	Gln	Gln	Arg	Glu	Ala	Glu	Arg	Lys	Ala	Gln	Lys	Glu		
	385				390					395					400		
aag	gaa	gag	tgg	gag	cgg	aaa	cag	aga	gaa	ctg	caa	gag	caa	gaa	tgg		1248
Lys	Glu	Glu	Trp	Glu	Arg	Lys	Gln	Arg	Glu	Leu	Gln	Glu	Gln	Glu	Trp		
			405						410					415			
aag	aag	cag	ctg	gag	ttg	gag	aaa	cgc	ttg	gag	aaa	cag	aga	gag	ctg		1296
Lys	Lys	Gln	Leu	Glu	Leu	Glu	Lys	Arg	Leu	Glu	Lys	Gln	Arg	Glu	Leu		
		420						425				430					
gag	aga	cag	cgg	gag	gaa	gag	agg	aga	aag	gag	ata	gaa	aga	cga	gag		1344
Glu	Arg	Gln	Arg	Glu	Glu	Glu	Arg	Arg	Lys	Glu	Ile	Glu	Arg	Arg	Glu		
		435					440					445					
gca	gca	aaa	cag	gag	ctt	gag	aga	caa	cgc	cgt	tta	gaa	tgg	gaa	aga		1392
Ala	Ala	Lys	Gln	Glu	Leu	Glu	Arg	Gln	Arg	Arg	Leu	Glu	Trp	Glu	Arg		
	450					455					460						
ctc	cgt	cgg	cag	gag	ctg	ctc	agt	cag	aag	acc	agg	gaa	caa	gaa	gac		1440
Leu	Arg	Arg	Gln	Glu	Leu	Leu	Ser	Gln	Lys	Thr	Arg	Glu	Gln	Glu	Asp		
	465				470					475					480		
att	gtc	agg	ctg	agc	tcc	aga	aag	aaa	agt	ctc	cac	ctg	gaa	ctg	gaa		1488
Ile	Val	Arg	Leu	Ser	Ser	Arg	Lys	Lys	Ser	Leu	His	Leu	Glu	Leu	Glu		
			485						490					495			
gca	gtg	aat	gga	aaa	cat	cag	cag	atc	tca	ggc	aga	cta	caa	gat	gtc		1536
Ala	Val	Asn	Gly	Lys	His	Gln	Gln	Ile	Ser	Gly	Arg	Leu	Gln	Asp	Val		
		500						505				510					
caa	atc	aga	aag	caa	aca	caa	aag	act	gag	cta	gaa	gtt	ttg	gat	aaa		1584
Gln	Ile	Arg	Lys	Gln	Thr	Gln	Lys	Thr	Glu	Leu	Glu	Val	Leu	Asp	Lys		
		515					520					525					
cag	tgt	gac	ctg	gaa	att	atg	gaa	atc	aaa	caa	ctt	caa	caa	gag	ctt		1632
Gln	Cys	Asp	Leu	Glu	Ile	Met	Glu	Ile	Lys	Gln	Leu	Gln	Gln	Glu	Leu		
	530					535					540						
aag	gaa	tat	caa	aat	aag	ctt	atc	tat	ctg	gtc	cct	gag	aag	cag	cta		1680
Lys	Glu	Tyr	Gln	Asn	Lys	Leu	Ile	Tyr	Leu	Val	Pro	Glu	Lys	Gln	Leu		
	545				550					555					560		
tta	aac	gaa	aga	att	aaa	aac	atg	cag	ctc	agt	aac	aca	cct	gat	tca		1728
Leu	Asn	Glu	Arg	Ile	Lys	Asn	Met	Gln	Leu	Ser	Asn	Thr	Pro	Asp	Ser		
			565					570						575			
ggg	atc	agt	tta	ctt	cat	aaa	aag	tca	tca	gaa	aag	gaa	gaa	tta	tgc		1776
Gly	Ile	Ser	Leu	Leu	His	Lys	Lys	Ser	Ser	Glu	Lys	Glu	Glu	Leu	Cys		

580	585	590	
caa aga ctt aaa gaa caa tta gat gct ctt gaa aaa gaa act gca tct Gln Arg Leu Lys Glu Gln Leu Asp Ala Leu Glu Lys Glu Thr Ala Ser 595 600 605			1824
aag ctc tca gaa atg gat tca ttt aac aat cag ctg aag gaa ctc aga Lys Leu Ser Glu Met Asp Ser Phe Asn Asn Gln Leu Lys Glu Leu Arg 610 615 620			1872
gaa agc tat aat aca cag cag tta gcc ctt gaa caa ctt cat aaa atc Glu Ser Tyr Asn Thr Gln Gln Leu Ala Leu Glu Gln Leu His Lys Ile 625 630 635 640			1920
aaa cgt gac aaa ttg aag gaa atc gaa aga aaa aga tta gag caa att Lys Arg Asp Lys Leu Lys Glu Ile Glu Arg Lys Arg Leu Glu Gln Ile 645 650 655			1968
caa aaa aag aaa cta gaa gat gag gct gca agg aaa gca aag caa gga Gln Lys Lys Lys Leu Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly 660 665 670			2016
aaa gaa aac ttg tgg aga gaa agt att aga aag gaa gaa gag gaa aag Lys Glu Asn Leu Trp Arg Glu Ser Ile Arg Lys Glu Glu Glu Glu Lys 675 680 685			2064
caa aaa cga ctc cag gaa gaa aag tca cag gac aaa act caa gaa gag Gln Lys Arg Leu Gln Glu Glu Lys Ser Gln Asp Lys Thr Gln Glu Glu 690 695 700			2112
gaa cga aaa gct gag gca aaa caa agt gag aca gcc agt gct ttg gtg Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val 705 710 715 720			2160
aat tac aga gca ctg tac cct ttt gaa gca aga aac cat gat gag atg Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met 725 730 735			2208
agt ttt agt tct ggg gat ata att cag gtt gat gaa aaa act gta gga Ser Phe Ser Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly 740 745 750			2256
gag cct ggt tgg ctt tat ggt agt ttt cag gga aag ttt ggc tgg ttc Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe 755 760 765			2304
ccc tgc aac tat gta gaa aaa gtg ctg tca agt gaa aaa gct ctg tct Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser 770 775 780			2352
cct aag aag gcc tta ctt cct cct aca gtg tct ctc tct gct acc tca Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser 785 790 795 800			2400
act tct tcc cag cca cca gca tca gtg act gat tat cac aat gta tcc Thr Ser Ser Gln Pro Pro Ala Ser Val Thr Asp Tyr His Asn Val Ser 805 810 815			2448

ttc tca aac ctt act gtt aat aca aca tgg cag cag aag tca gct ttt	2496
Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe	
820 825 830	
acc cgc act gtg tcc cct gga tct gtg tcc ccc att cac gga cag ggg	2544
Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly	
835 840 845	
cag gct gta gaa aac ctg aaa gcc cag gcc ctt tgt tcc tgg acg gca	2592
Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala	
850 855 860	
aag aag gag aac cac ctg aac ttc tca aag cac gac gtc atc act gtc	2640
Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val	
865 870 875 880	
ctg gag cag cag gaa aac tgg tgg ttt ggg gag gtg cac gga gga aga	2688
Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg	
885 890 895	
gga tgg ttc ccc aag tct tat gtc aag ctc att cct ggg aat gaa gta	2736
Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val	
900 905 910	
cag cga gga gag cca gaa gct ttg tat gca gct gtg act aag aaa cct	2784
Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro	
915 920 925	
acc tcc aca gcc tat cca gtt acc tcc aca gcc tat cca gtt gga gaa	2832
Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu	
930 935 940	
gac tac att gca ctt tat tca tac tca agt gta gag ccc ggg gat ttg	2880
Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Ser Val Glu Pro Gly Asp Leu	
945 950 955 960	
act ttc act gaa ggt gaa gaa att cta gtg acc cag aaa gat gga gag	2928
Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys Asp Gly Glu	
965 970 975	
tgg tgg aca gga agt att gga gag aga act gga atc ttc ccg tcc aac	2976
Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn	
980 985 990	
tac gtc aga cca aag gat caa gag aat ttt ggg aat gct agc aaa tct	3024
Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser	
995 1000 1005	
gga gca tca aac aaa aaa ccc gag atc gct caa gta act tca gca	3069
Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala	
1010 1015 1020	
tat gct gct tca ggg act gag cag ctc agc ctt gcg cca gga cag	3114
Tyr Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln	
1025 1030 1035	

tta ata tta atc tta aag aaa aac aca agc ggg tgg tgg caa gga	3159
Leu Ile Leu Ile Leu Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly	
1040 1045 1050	
gag cta cag gcc aga ggg aag aaa cga cag aag gga tgg ttt cct	3204
Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Lys Gly Trp Phe Pro	
1055 1060 1065	
gcc agc cat gta aag ctg cta ggt cca agc agt gaa aga acc atg	3249
Ala Ser His Val Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met	
1070 1075 1080	
cct act ttt cac gct gta tgt caa gtg att gct atg tat gac tac	3294
Pro Thr Phe His Ala Val Cys Gln Val Ile Ala Met Tyr Asp Tyr	
1085 1090 1095	
atg gcg aat aac gaa gat gag ctc aat ttc tcc aaa gga cag ctg	3339
Met Ala Asn Asn Glu Asp Glu Leu Asn Phe Ser Lys Gly Gln Leu	
1100 1105 1110	
att aat gtt atg aac aaa gat gac cct gac tgg tgg caa gga gaa	3384
Ile Asn Val Met Asn Lys Asp Asp Pro Asp Trp Trp Gln Gly Glu	
1115 1120 1125	
acc aat ggt ctg act ggt ctc ttt cct tca aac tat gtt aag atg	3429
Thr Asn Gly Leu Thr Gly Leu Phe Pro Ser Asn Tyr Val Lys Met	
1130 1135 1140	
aca aca gac tca gat cca agt caa cag tgg tgt gct gac ctc caa	3474
Thr Thr Asp Ser Asp Pro Ser Gln Gln Trp Cys Ala Asp Leu Gln	
1145 1150 1155	
gcc ctg gac aca atg cag cct acg gag agg aag cga cag ggc tac	3519
Ala Leu Asp Thr Met Gln Pro Thr Glu Arg Lys Arg Gln Gly Tyr	
1160 1165 1170	
att cac gag ctc att cag aca gag gag cgg tac atg gac gac gac	3564
Ile His Glu Leu Ile Gln Thr Glu Glu Arg Tyr Met Asp Asp Asp	
1175 1180 1185	
ctg cag ctg gtc atc gag gtc ttc cag aaa cgg atg gct gag gaa	3609
Leu Gln Leu Val Ile Glu Val Phe Gln Lys Arg Met Ala Glu Glu	
1190 1195 1200	
ggc ttc ctc act gaa gca gac atg gct ctg atc ttt gtg aac tgg	3654
Gly Phe Leu Thr Glu Ala Asp Met Ala Leu Ile Phe Val Asn Trp	
1205 1210 1215	
aaa gag ctc atc atg tcc aac acg aag ctg ctg agg gcc ttg cgg	3699
Lys Glu Leu Ile Met Ser Asn Thr Lys Leu Leu Arg Ala Leu Arg	
1220 1225 1230	
gtg agg aag aag act ggg ggt gag aag atg cca gtt cag atg att	3744
Val Arg Lys Lys Thr Gly Gly Glu Lys Met Pro Val Gln Met Ile	
1235 1240 1245	
gga gac atc ctg gcg gca gag ctg tcc cac atg cag gcc tac atc	3789

Gly	Asp	Ile	Leu	Ala	Ala	Glu	Leu	Ser	His	Met	Gln	Ala	Tyr	Ile		
1250						1255					1260					
cgc	ttc	tgc	agc	tgt	cag	ctt	aat	ggg	gca	acc	ctg	tta	cag	cag	3834	
Arg	Phe	Cys	Ser	Cys	Gln	Leu	Asn	Gly	Ala	Thr	Leu	Leu	Gln	Gln		
1265						1270					1275					
aag	aca	gac	gag	gac	acg	gac	ttc	aag	gaa	ttt	cta	aag	aag	ttg	3879	
Lys	Thr	Asp	Glu	Asp	Thr	Asp	Phe	Lys	Glu	Phe	Leu	Lys	Lys	Leu		
1280						1285					1290					
gca	tca	gac	cca	cga	tgc	aaa	ggg	atg	ccc	ctc	tcc	agc	ttc	ctg	3924	
Ala	Ser	Asp	Pro	Arg	Cys	Lys	Gly	Met	Pro	Leu	Ser	Ser	Phe	Leu		
1295						1300					1305					
ctg	aag	ccc	atg	cag	agg	atc	act	cgc	tac	ccg	ctg	ctc	atc	cga	3969	
Leu	Lys	Pro	Met	Gln	Arg	Ile	Thr	Arg	Tyr	Pro	Leu	Leu	Ile	Arg		
1310						1315					1320					
agt	atc	ctg	gag	aac	act	cca	cag	agt	cat	gtt	gac	cac	tcc	tcc	4014	
Ser	Ile	Leu	Glu	Asn	Thr	Pro	Gln	Ser	His	Val	Asp	His	Ser	Ser		
1325						1330					1335					
ctg	aag	ctg	gcc	cta	gaa	cgt	gct	gag	gag	ctg	tgc	tct	cag	gtg	4059	
Leu	Lys	Leu	Ala	Leu	Glu	Arg	Ala	Glu	Glu	Leu	Cys	Ser	Gln	Val		
1340						1345					1350					
aac	gag	gga	gtc	cgg	gag	aag	gaa	aat	tca	gac	cgg	ctg	gag	tgg	4104	
Asn	Glu	Gly	Val	Arg	Glu	Lys	Glu	Asn	Ser	Asp	Arg	Leu	Glu	Trp		
1355						1360					1365					
atc	cag	gca	cac	gtg	cag	tgc	gaa	ggc	ttg	gca	gag	caa	ctt	att	4149	
Ile	Gln	Ala	His	Val	Gln	Cys	Glu	Gly	Leu	Ala	Glu	Gln	Leu	Ile		
1370						1375					1380					
ttc	aac	tcc	ctc	acc	aac	tgc	ctg	ggc	ccc	cgg	aag	ctt	ctg	cac	4194	
Phe	Asn	Ser	Leu	Thr	Asn	Cys	Leu	Gly	Pro	Arg	Lys	Leu	Leu	His		
1385						1390					1395					
agc	ggg	aag	ctg	tac	aag	acc	aag	agc	aat	aag	gag	ctg	cac	gcc	4239	
Ser	Gly	Lys	Leu	Tyr	Lys	Thr	Lys	Ser	Asn	Lys	Glu	Leu	His	Ala		
1400						1405					1410					
ttc	ctc	ttc	aac	gac	ttc	ctg	ctg	ctc	acc	tac	ctg	gtc	agg	cag	4284	
Phe	Leu	Phe	Asn	Asp	Phe	Leu	Leu	Leu	Thr	Tyr	Leu	Val	Arg	Gln		
1415						1420					1425					
ttt	gcc	gcc	gcc	tct	ggc	cac	gag	aag	ctc	ttc	aac	tcc	aag	tcc	4329	
Phe	Ala	Ala	Ala	Ser	Gly	His	Glu	Lys	Leu	Phe	Asn	Ser	Lys	Ser		
1430						1435					1440					
agt	gct	cag	ttc	cgg	atg	tac	aaa	acg	ccc	att	ttc	ctg	aat	gaa	4374	
Ser	Ala	Gln	Phe	Arg	Met	Tyr	Lys	Thr	Pro	Ile	Phe	Leu	Asn	Glu		
1445						1450					1455					
gtg	ttg	gtg	aaa	ctt	ccc	aca	gac	cct	tcc	ggc	gat	gag	ccc	gtc	4419	
Val	Leu	Val	Lys	Leu	Pro	Thr	Asp	Pro	Ser	Gly	Asp	Glu	Pro	Val		

1460	1465	1470	
ttc cac att tcc cac att gat	cgt gtg tac aca ctc	cga aca gac	4464
Phe His Ile Ser His Ile Asp	Arg Val Tyr Thr Leu	Arg Thr Asp	
1475	1480	1485	
aac atc aac gag agg acg gcc	tgg gtc cag aag atc	aag ggt gcc	4509
Asn Ile Asn Glu Arg Thr Ala	Trp Val Gln Lys Ile	Lys Gly Ala	
1490	1495	1500	
tca gag cag tac atc gac act	gag aag aag aaa cgg	gaa aag gct	4554
Ser Glu Gln Tyr Ile Asp Thr	Glu Lys Lys Lys Arg	Glu Lys Ala	
1505	1510	1515	
tac caa gcc cgt tct caa aag	act tca ggt att ggg	cgt ctg atg	4599
Tyr Gln Ala Arg Ser Gln Lys	Thr Ser Gly Ile Gly	Arg Leu Met	
1520	1525	1530	
gtg cat gtc att gaa gct aca	gaa tta aaa gcc tgc	aaa cca aac	4644
Val His Val Ile Glu Ala Thr	Glu Leu Lys Ala Cys	Lys Pro Asn	
1535	1540	1545	
ggg aaa agt aat cca tac tgt	gaa gtc agc atg ggc	tcc caa agc	4689
Gly Lys Ser Asn Pro Tyr Cys	Glu Val Ser Met Gly	Ser Gln Ser	
1550	1555	1560	
tat acc acc agg acc ctg cag	gac aca cta aac ccc	aag tgg aac	4734
Tyr Thr Thr Arg Thr Leu Gln	Asp Thr Leu Asn Pro	Lys Trp Asn	
1565	1570	1575	
ttc aac tgc cag ttc ttc atc	aag gat ctt tac cag	gac gtt ctg	4779
Phe Asn Cys Gln Phe Phe Ile	Lys Asp Leu Tyr Gln	Asp Val Leu	
1580	1585	1590	
tgt ctc act atg ttt gac aga	gac cag ttt tct cca	gat gac ttc	4824
Cys Leu Thr Met Phe Asp Arg	Asp Gln Phe Ser Pro	Asp Asp Phe	
1595	1600	1605	
ttg ggt cgt act gaa gtt cca	gtg gca aaa atc cga	aca gaa cag	4869
Leu Gly Arg Thr Glu Val Pro	Val Ala Lys Ile Arg	Thr Glu Gln	
1610	1615	1620	
gaa agc aaa ggc ccc acc acc	cgc cga cta cta ctg	cac gaa gtc	4914
Glu Ser Lys Gly Pro Thr Thr	Arg Arg Leu Leu Leu	His Glu Val	
1625	1630	1635	
ccc act gga gaa gtc tgg gtc	cgc ttt gac ctg caa	ctt ttt gaa	4959
Pro Thr Gly Glu Val Trp Val	Arg Phe Asp Leu Gln	Leu Phe Glu	
1640	1645	1650	
caa aaa act ctc ctt tga			4977
Gln Lys Thr Leu Leu			
1655			

<210> 27  
<211> 1658



<212> PRT

<213> Mus musculus

<400> 27

Met Ala Gln Phe Pro Thr Ala Met Asn Gly Gly Pro Asn Met Trp Ala  
1 5 10 15

Ile Thr Ser Glu Glu Arg Thr Lys His Asp Lys Gln Phe Asp Asn Leu  
20 25 30

Lys Pro Ser Gly Gly Tyr Ile Thr Gly Asp Gln Ala Arg Thr Phe Phe  
35 40 45

Leu Gln Ser Gly Leu Pro Ala Pro Val Leu Ala Glu Ile Trp Ala Leu  
50 55 60

Ser Asp Leu Asn Lys Asp Gly Lys Met Asp Gln Gln Glu Phe Ser Ile  
65 70 75 80

Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Gln Gln Leu Pro Val  
85 90 95

Val Leu Pro Pro Ile Met Lys Gln Pro Pro Met Phe Ser Pro Leu Ile  
100 105 110

Ser Ala Arg Phe Gly Met Gly Ser Met Pro Asn Leu Ser Ile His Gln  
115 120 125

Pro Leu Pro Pro Val Ala Pro Ile Ala Thr Pro Leu Ser Ser Ala Thr  
130 135 140

Ser Gly Thr Ser Ile Pro Pro Leu Met Met Pro Ala Pro Leu Val Pro  
145 150 155 160

Ser Val Ser Thr Ser Ser Leu Pro Asn Gly Thr Ala Ser Leu Ile Gln  
165 170 175

Pro Leu Ser Ile Pro Tyr Ser Ser Ser Thr Leu Pro His Ala Ser Ser  
180 185 190

Tyr Ser Leu Met Met Gly Gly Phe Gly Gly Ala Ser Ile Gln Lys Ala  
195 200 205

Gln Ser Leu Ile Asp Leu Gly Ser Ser Ser Ser Thr Ser Ser Thr Ala  
 210 215 220

Ser Leu Ser Gly Asn Ser Pro Lys Thr Gly Thr Ser Glu Trp Ala Val  
 225 230 235 240

Pro Gln Pro Ser Arg Leu Lys Tyr Arg Gln Lys Phe Asn Ser Leu Asp  
 245 250 255

Lys Gly Met Ser Gly Tyr Leu Ser Gly Phe Gln Ala Arg Asn Ala Leu  
 260 265 270

Leu Gln Ser Asn Leu Ser Gln Thr Gln Leu Ala Thr Ile Trp Thr Leu  
 275 280 285

Ala Asp Ile Asp Gly Asp Gly Gln Leu Lys Ala Glu Glu Phe Ile Leu  
 290 295 300

Ala Met His Leu Thr Asp Met Ala Lys Ala Gly Gln Pro Leu Pro Leu  
 305 310 315 320

Thr Leu Pro Pro Glu Leu Val Pro Pro Ser Phe Arg Gly Gly Lys Gln  
 325 330 335

Val Asp Ser Val Asn Gly Thr Leu Pro Ser Tyr Gln Lys Thr Gln Glu  
 340 345 350

Glu Glu Pro Gln Lys Lys Leu Pro Val Thr Phe Glu Asp Lys Arg Lys  
 355 360 365

Ala Asn Tyr Glu Arg Gly Asn Met Glu Leu Glu Lys Arg Arg Gln Val  
 370 375 380

Leu Met Glu Gln Gln Gln Arg Glu Ala Glu Arg Lys Ala Gln Lys Glu  
 385 390 395 400

Lys Glu Glu Trp Glu Arg Lys Gln Arg Glu Leu Gln Glu Gln Glu Trp  
 405 410 415

Lys Lys Gln Leu Glu Leu Glu Lys Arg Leu Glu Lys Gln Arg Glu Leu  
 420 425 430

Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg Arg Glu

435		440		445
Ala Ala Lys Gln Glu Leu Glu Arg Gln Arg Arg Leu Glu Trp Glu Arg				
450		455		460
Leu Arg Arg Gln Glu Leu Leu Ser Gln Lys Thr Arg Glu Gln Glu Asp				
465		470		475 480
Ile Val Arg Leu Ser Ser Arg Lys Lys Ser Leu His Leu Glu Leu Glu				
		485		490 495
Ala Val Asn Gly Lys His Gln Gln Ile Ser Gly Arg Leu Gln Asp Val				
		500		505 510
Gln Ile Arg Lys Gln Thr Gln Lys Thr Glu Leu Glu Val Leu Asp Lys				
		515		520 525
Gln Cys Asp Leu Glu Ile Met Glu Ile Lys Gln Leu Gln Gln Glu Leu				
		530		535 540
Lys Glu Tyr Gln Asn Lys Leu Ile Tyr Leu Val Pro Glu Lys Gln Leu				
545		550		555 560
Leu Asn Glu Arg Ile Lys Asn Met Gln Leu Ser Asn Thr Pro Asp Ser				
		565		570 575
Gly Ile Ser Leu Leu His Lys Lys Ser Ser Glu Lys Glu Glu Leu Cys				
		580		585 590
Gln Arg Leu Lys Glu Gln Leu Asp Ala Leu Glu Lys Glu Thr Ala Ser				
		595		600 605
Lys Leu Ser Glu Met Asp Ser Phe Asn Asn Gln Leu Lys Glu Leu Arg				
		610		615 620
Glu Ser Tyr Asn Thr Gln Gln Leu Ala Leu Glu Gln Leu His Lys Ile				
625		630		635 640
Lys Arg Asp Lys Leu Lys Glu Ile Glu Arg Lys Arg Leu Glu Gln Ile				
		645		650 655
Gln Lys Lys Lys Leu Glu Asp Glu Ala Ala Arg Lys Ala Lys Gln Gly				
		660		665 670

Lys Glu Asn Leu Trp Arg Glu Ser Ile Arg Lys Glu Glu Glu Glu Lys  
675 680 685

Gln Lys Arg Leu Gln Glu Glu Lys Ser Gln Asp Lys Thr Gln Glu Glu  
690 695 700

Glu Arg Lys Ala Glu Ala Lys Gln Ser Glu Thr Ala Ser Ala Leu Val  
705 710 715 720

Asn Tyr Arg Ala Leu Tyr Pro Phe Glu Ala Arg Asn His Asp Glu Met  
725 730 735

Ser Phe Ser Ser Gly Asp Ile Ile Gln Val Asp Glu Lys Thr Val Gly  
740 745 750

Glu Pro Gly Trp Leu Tyr Gly Ser Phe Gln Gly Lys Phe Gly Trp Phe  
755 760 765

Pro Cys Asn Tyr Val Glu Lys Val Leu Ser Ser Glu Lys Ala Leu Ser  
770 775 780

Pro Lys Lys Ala Leu Leu Pro Pro Thr Val Ser Leu Ser Ala Thr Ser  
785 790 795 800

Thr Ser Ser Gln Pro Pro Ala Ser Val Thr Asp Tyr His Asn Val Ser  
805 810 815

Phe Ser Asn Leu Thr Val Asn Thr Thr Trp Gln Gln Lys Ser Ala Phe  
820 825 830

Thr Arg Thr Val Ser Pro Gly Ser Val Ser Pro Ile His Gly Gln Gly  
835 840 845

Gln Ala Val Glu Asn Leu Lys Ala Gln Ala Leu Cys Ser Trp Thr Ala  
850 855 860

Lys Lys Glu Asn His Leu Asn Phe Ser Lys His Asp Val Ile Thr Val  
865 870 875 880

Leu Glu Gln Gln Glu Asn Trp Trp Phe Gly Glu Val His Gly Gly Arg  
885 890 895

Gly Trp Phe Pro Lys Ser Tyr Val Lys Leu Ile Pro Gly Asn Glu Val  
 900 905 910

Gln Arg Gly Glu Pro Glu Ala Leu Tyr Ala Ala Val Thr Lys Lys Pro  
 915 920 925

Thr Ser Thr Ala Tyr Pro Val Thr Ser Thr Ala Tyr Pro Val Gly Glu  
 930 935 940

Asp Tyr Ile Ala Leu Tyr Ser Tyr Ser Ser Val Glu Pro Gly Asp Leu  
 945 950 955 960

Thr Phe Thr Glu Gly Glu Glu Ile Leu Val Thr Gln Lys Asp Gly Glu  
 965 970 975

Trp Trp Thr Gly Ser Ile Gly Glu Arg Thr Gly Ile Phe Pro Ser Asn  
 980 985 990

Tyr Val Arg Pro Lys Asp Gln Glu Asn Phe Gly Asn Ala Ser Lys Ser  
 995 1000 1005

Gly Ala Ser Asn Lys Lys Pro Glu Ile Ala Gln Val Thr Ser Ala  
 1010 1015 1020

Tyr Ala Ala Ser Gly Thr Glu Gln Leu Ser Leu Ala Pro Gly Gln  
 1025 1030 1035

Leu Ile Leu Ile Leu Lys Lys Asn Thr Ser Gly Trp Trp Gln Gly  
 1040 1045 1050

Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Lys Gly Trp Phe Pro  
 1055 1060 1065

Ala Ser His Val Lys Leu Leu Gly Pro Ser Ser Glu Arg Thr Met  
 1070 1075 1080

Pro Thr Phe His Ala Val Cys Gln Val Ile Ala Met Tyr Asp Tyr  
 1085 1090 1095

Met Ala Asn Asn Glu Asp Glu Leu Asn Phe Ser Lys Gly Gln Leu  
 1100 1105 1110

Ile	Asn	Val	Met	Asn	Lys	Asp	Asp	Pro	Asp	Trp	Trp	Gln	Gly	Glu
1115						1120					1125			
Thr	Asn	Gly	Leu	Thr	Gly	Leu	Phe	Pro	Ser	Asn	Tyr	Val	Lys	Met
1130						1135					1140			
Thr	Thr	Asp	Ser	Asp	Pro	Ser	Gln	Gln	Trp	Cys	Ala	Asp	Leu	Gln
1145						1150					1155			
Ala	Leu	Asp	Thr	Met	Gln	Pro	Thr	Glu	Arg	Lys	Arg	Gln	Gly	Tyr
1160						1165					1170			
Ile	His	Glu	Leu	Ile	Gln	Thr	Glu	Glu	Arg	Tyr	Met	Asp	Asp	Asp
1175						1180					1185			
Leu	Gln	Leu	Val	Ile	Glu	Val	Phe	Gln	Lys	Arg	Met	Ala	Glu	Glu
1190						1195					1200			
Gly	Phe	Leu	Thr	Glu	Ala	Asp	Met	Ala	Leu	Ile	Phe	Val	Asn	Trp
1205						1210					1215			
Lys	Glu	Leu	Ile	Met	Ser	Asn	Thr	Lys	Leu	Leu	Arg	Ala	Leu	Arg
1220						1225					1230			
Val	Arg	Lys	Lys	Thr	Gly	Gly	Glu	Lys	Met	Pro	Val	Gln	Met	Ile
1235						1240					1245			
Gly	Asp	Ile	Leu	Ala	Ala	Glu	Leu	Ser	His	Met	Gln	Ala	Tyr	Ile
1250						1255					1260			
Arg	Phe	Cys	Ser	Cys	Gln	Leu	Asn	Gly	Ala	Thr	Leu	Leu	Gln	Gln
1265						1270					1275			
Lys	Thr	Asp	Glu	Asp	Thr	Asp	Phe	Lys	Glu	Phe	Leu	Lys	Lys	Leu
1280						1285					1290			
Ala	Ser	Asp	Pro	Arg	Cys	Lys	Gly	Met	Pro	Leu	Ser	Ser	Phe	Leu
1295						1300					1305			
Leu	Lys	Pro	Met	Gln	Arg	Ile	Thr	Arg	Tyr	Pro	Leu	Leu	Ile	Arg
1310						1315					1320			
Ser	Ile	Leu	Glu	Asn	Thr	Pro	Gln	Ser	His	Val	Asp	His	Ser	Ser

1325		1330		1335
Leu Lys	Leu Ala	Leu Glu	Arg Ala	Glu Glu
1340			1345	Leu Cys
				1350
Asn Glu	Gly Val	Arg Glu	Lys Glu	Asn Ser
1355			1360	Asp Arg
				1365
Ile Gln	Ala His	Val Gln	Cys Glu	Gly Leu
1370			1375	Ala Glu
				1380
Phe Asn	Ser Leu	Thr Asn	Cys Leu	Gly Pro
1385			1390	Arg Lys
				1395
Ser Gly	Lys Leu	Tyr Lys	Thr Lys	Ser Asn
1400			1405	Lys Glu
				1410
Phe Leu	Phe Asn	Asp Phe	Leu Leu	Thr Tyr
1415			1420	Leu Val
				1425
Phe Ala	Ala Ala	Ser Gly	His Glu	Lys Leu
1430			1435	Phe Asn
				1440
Ser Ala	Gln Phe	Arg Met	Tyr Lys	Thr Pro
1445			1450	Ile Phe
				1455
Val Leu	Val Lys	Leu Pro	Thr Asp	Pro Ser
1460			1465	Gly Asp
				1470
Phe His	Ile Ser	His Ile	Asp Arg	Val Tyr
1475			1480	Thr Leu
				1485
Asn Ile	Asn Glu	Arg Thr	Ala Trp	Val Gln
1490			1495	Lys Ile
				1500
Ser Glu	Gln Tyr	Ile Asp	Thr Glu	Lys Lys
1505			1510	Lys Arg
				1515
Tyr Gln	Ala Arg	Ser Gln	Lys Thr	Ser Gly
1520			1525	Ile Gly
				1530
Val His	Val Ile	Glu Ala	Thr Glu	Leu Lys
1535			1540	Ala Cys
				1545

Gly Lys Ser Asn Pro Tyr Cys Glu Val Ser Met Gly Ser Gln Ser  
 1550 1555 1560

Tyr Thr Thr Arg Thr Leu Gln Asp Thr Leu Asn Pro Lys Trp Asn  
 1565 1570 1575

Phe Asn Cys Gln Phe Phe Ile Lys Asp Leu Tyr Gln Asp Val Leu  
 1580 1585 1590

Cys Leu Thr Met Phe Asp Arg Asp Gln Phe Ser Pro Asp Asp Phe  
 1595 1600 1605

Leu Gly Arg Thr Glu Val Pro Val Ala Lys Ile Arg Thr Glu Gln  
 1610 1615 1620

Glu Ser Lys Gly Pro Thr Thr Arg Arg Leu Leu Leu His Glu Val  
 1625 1630 1635

Pro Thr Gly Glu Val Trp Val Arg Phe Asp Leu Gln Leu Phe Glu  
 1640 1645 1650

Gln Lys Thr Leu Leu  
 1655

<210> 28  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 28  
 gaaggagaac tcagaccggc tggagtggat

30

<210> 29  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 29  
 gacagaggag cgtacatgg a

21



<210> 30  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 30  
 agctcccctg gttctggctt c 21

<210> 31  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 31  
 gaattcagaa ccatggaaca aaagcttatt tctgaagaag acttggggcc c 51

<210> 32  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 32  
 cctggattac aaggatgatg atgacaaatg actcgag 37

<210> 33  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Peptide  
  
 <400> 33

Met Ala Gln Phe Pro Thr Pro Phe Gly Gly Ser Leu Asp Val Trp Ala  
 1 5 10 15

Ile Thr Val Glu Glu  
 20

<210> 34  
 <211> 1270

<212> PRT

<213> *Xenopus laevis*

<400> 34

Met Ala Gln Phe Gly Thr Pro Phe Gly Gly Asn Leu Asp Ile Trp Ala  
1 5 10 15

Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe His Gly Leu  
20 25 30

Lys Pro Thr Ala Gly Tyr Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe  
35 40 45

Leu Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu  
50 55 60

Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Leu Glu Phe Ser Ile  
65 70 75 80

Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Tyr Pro Leu Pro Ser  
85 90 95

Ile Leu Pro Ser Asn Met Leu Lys Gln Pro Val Ala Met Pro Ala Ala  
100 105 110

Ala Val Ala Gly Phe Gly Met Ser Gly Ile Val Gly Ile Pro Pro Leu  
115 120 125

Ala Ala Val Ala Pro Val Pro Met Pro Ser Ile Pro Val Val Gly Met  
130 135 140

Ser Pro Pro Leu Val Ser Ser Val Pro Thr Val Pro Pro Leu Ser Asn  
145 150 155 160

Gly Ala Pro Ala Val Ile Gln Ser His Pro Ala Phe Ala His Ser Ala  
165 170 175

Thr Leu Pro Lys Ser Ser Ser Phe Gly Arg Ser Val Ala Gly Ser Gln  
180 185 190

Ile Asn Thr Lys Leu Gln Lys Ala Gln Ser Phe Asp Val Pro Ala Pro  
195 200 205

Pro Leu Val Val Glu Trp Ala Val Pro Ser Ser Ser Arg Leu Lys Tyr  
 210 215 220

Arg Gln Leu Phe Asn Ser Gln Asp Lys Thr Met Ser Gly Asn Leu Thr  
 225 230 235 240

Gly Pro Gln Ala Arg Thr Ile Leu Met Gln Ser Ser Leu Pro Gln Ser  
 245 250 255

Gln Leu Ala Thr Ile Trp Asn Leu Ser Asp Ile Asp Gln Asp Gly Lys  
 260 265 270

Leu Thr Ala Glu Glu Phe Ile Leu Ala Met His Leu Ile Asp Val Ala  
 275 280 285

Met Ser Gly Gln Pro Leu Pro Pro Ile Leu Pro Pro Glu Tyr Ile Pro  
 290 295 300

Pro Ser Phe Arg Arg Val Arg Ser Gly Ser Gly Leu Ser Ile Met Ser  
 305 310 315 320

Ser Val Ser Val Asp Gln Arg Leu Pro Glu Glu Pro Glu Glu Glu Glu  
 325 330 335

Pro Gln Asn Ala Asp Lys Lys Leu Pro Val Thr Phe Glu Asp Lys Lys  
 340 345 350

Arg Glu Asn Phe Glu Arg Gly Asn Leu Glu Leu Glu Lys Arg Arg Gln  
 355 360 365

Ala Leu Leu Glu Gln Gln Arg Lys Glu Gln Glu Arg Leu Ala Gln Leu  
 370 375 380

Glu Arg Ala Glu Gln Glu Arg Lys Glu Arg Glu Arg Gln Asp Gln Glu  
 385 390 395 400

Arg Lys Arg Gln Gln Asp Leu Glu Lys Gln Leu Glu Lys Gln Arg Glu  
 405 410 415

Leu Glu Arg Gln Arg Glu Glu Glu Arg Arg Lys Glu Ile Glu Arg Arg  
 420 425 430

Glu Ala Ala Lys Arg Glu Leu Glu Arg Gln Arg Gln Leu Glu Trp Glu

435		440		445
Arg Asn Arg Arg Gln Glu Leu Leu Asn Gln Arg Asn Arg Glu Gln Glu				
450		455		460
Asp Ile Val Val Leu Lys Ala Lys Lys Lys Thr Leu Glu Phe Glu Leu				
465		470		475 480
Glu Ala Leu Asn Asp Lys Lys His Gln Leu Glu Gly Lys Leu Gln Asp				
		485		490 495
Ile Arg Cys Arg Leu Thr Thr Gln Arg His Glu Ile Glu Ser Thr Asn				
		500		505 510
Lys Ser Arg Glu Leu Arg Ile Ala Glu Ile Thr His Leu Gln Gln Gln				
		515		520 525
Leu Gln Glu Ser Gln Gln Leu Leu Gly Lys Met Ile Pro Glu Lys Gln				
		530		535 540
Ser Leu Ile Asp Gln Leu Lys Gln Val Gln Gln Asn Ser Leu His Arg				
		545		550 555 560
Asp Ser Leu Leu Thr Leu Lys Arg Ala Leu Glu Thr Lys Glu Ile Gly				
		565		570 575
Arg Gln Gln Leu Arg Asp Gln Leu Asp Glu Val Glu Lys Glu Thr Arg				
		580		585 590
Ala Lys Leu Gln Glu Ile Asp Val Phe Asn Asn Gln Leu Lys Glu Leu				
		595		600 605
Arg Glu Leu Tyr Asn Lys Gln Gln Phe Gln Lys Gln Gln Asp Phe Glu				
		610		615 620
Thr Glu Lys Ile Lys Gln Lys Glu Leu Glu Arg Lys Thr Ser Glu Leu				
		625		630 635 640
Asp Lys Leu Lys Glu Glu Asp Lys Arg Arg Met Leu Glu Gln Asp Lys				
		645		650 655
Leu Trp Gln Asp Arg Val Lys Gln Glu Glu Glu Arg Tyr Lys Phe Gln				
		660		665 670

Asp Glu Glu Lys Glu Lys Arg Glu Glu Ser Val Gln Lys Cys Glu Val  
675 680 685

Glu Lys Lys Pro Glu Ile Gln Glu Lys Pro Asn Lys Pro Phe His Gln  
690 695 700

Pro Pro Glu Pro Gly Lys Leu Gly Gly Gln Ile Pro Trp Met Asn Thr  
705 710 715 720

Glu Lys Ala Pro Leu Thr Ile Asn Gln Gly Asp Val Lys Val Val Tyr  
725 730 735

Tyr Arg Ala Leu Tyr Pro Phe Asp Ala Arg Ser His Asp Glu Ile Thr  
740 745 750

Ile Glu Pro Gly Asp Ile Ile Met Val Asp Glu Ser Gln Thr Gly Glu  
755 760 765

Pro Gly Trp Leu Gly Gly Glu Leu Lys Gly Lys Thr Gly Trp Phe Pro  
770 775 780

Ala Asn Tyr Ala Glu Arg Met Pro Glu Ser Glu Phe Pro Ser Thr Thr  
785 790 795 800

Lys Pro Ala Ala Glu Thr Thr Ala Lys Pro Thr Val His Val Ala Pro  
805 810 815

Ser Pro Val Ala Pro Ala Ala Phe Thr Asn Thr Ser Thr Asn Ser Asn  
820 825 830

Asn Trp Ala Asp Phe Ser Ser Thr Trp Pro Thr Asn Asn Thr Asp Lys  
835 840 845

Val Glu Ser Asp Asn Trp Asp Thr Trp Ala Ala Gln Pro Ser Leu Thr  
850 855 860

Val Pro Ser Ala Gly Gln His Arg Gln Arg Ser Ala Phe Thr Pro Ala  
865 870 875 880

Thr Val Thr Gly Ser Ser Pro Ser Pro Val Leu Gly Gln Gly Glu Lys  
885 890 895

Val Glu Gly Leu Gln Ala Gln Ala Leu Tyr Pro Trp Arg Ala Lys Lys  
900 905 910

Asp Asn His Leu Asn Phe Asn Lys Asn Asp Val Ile Thr Val Leu Glu  
915 920 925

Gln Gln Asp Met Trp Trp Phe Gly Glu Val Gln Gly Gln Lys Gly Trp  
930 935 940

Phe Pro Lys Ser Tyr Val Lys Leu Ile Ser Gly Pro Leu Arg Lys Ser  
945 950 955 960

Thr Ser Ile Asp Ser Thr Ser Ser Glu Ser Pro Ala Ser Leu Lys Arg  
965 970 975

Val Ser Ser Pro Ala Phe Lys Pro Ala Ile Gln Gly Glu Glu Tyr Ile  
980 985 990

Ser Met Tyr Thr Tyr Glu Ser Asn Glu Gln Gly Asp Leu Thr Phe Gln  
995 1000 1005

Gln Gly Asp Leu Ile Val Val Ile Lys Lys Asp Gly Asp Trp Trp  
1010 1015 1020

Thr Gly Thr Val Gly Glu Lys Thr Gly Val Phe Pro Ser Asn Tyr  
1025 1030 1035

Val Arg Pro Lys Asp Ser Glu Ala Ala Gly Ser Gly Gly Lys Thr  
1040 1045 1050

Gly Ser Leu Gly Lys Lys Pro Glu Ile Ala Gln Val Ile Ala Ser  
1055 1060 1065

Tyr Ala Ala Thr Ala Pro Glu Gln Leu Thr Leu Ala Pro Gly Gln  
1070 1075 1080

Leu Ile Leu Ile Arg Lys Lys Asn Pro Gly Gly Trp Trp Glu Gly  
1085 1090 1095

Glu Leu Gln Ala Arg Gly Lys Lys Arg Gln Ile Gly Trp Phe Pro  
1100 1105 1110

Ala Asn Tyr Val Lys Leu Leu Ser Pro Gly Thr Asn Lys Ser Thr  
 1115 1120 1125

Pro Thr Glu Pro Pro Lys Pro Thr Ser Leu Pro Pro Thr Cys Gln  
 1130 1135 1140

Val Ile Gly Met Tyr Asp Tyr Ile Ala Gln Asn Asp Asp Glu Leu  
 1145 1150 1155

Ala Phe Ser Lys Gly Gln Val Ile Asn Val Leu Asn Lys Glu Asp  
 1160 1165 1170

Pro Asp Trp Trp Lys Gly Glu Leu Asn Gly His Val Gly Leu Phe  
 1175 1180 1185

Pro Ser Asn Tyr Val Lys Leu Thr Thr Asp Met Asp Pro Ser Gln  
 1190 1195 1200

Gln Phe Arg Leu Gly Val Lys Pro Ala Gly Gly Ile Pro Ala Thr  
 1205 1210 1215

Gly Asp Arg Pro Phe Ile Leu Phe Pro Phe Arg Asp Gly Pro Ser  
 1220 1225 1230

Leu Leu Pro Asn Ala Phe Gln Ala Pro Pro Leu Ser Val Val Met  
 1235 1240 1245

Ile Lys Phe Arg Cys Phe Thr Ala Pro Arg Phe Cys Pro Asp Met  
 1250 1255 1260

Asn Val Lys Tyr Ile Asn Ile  
 1265 1270

<210> 35  
 <211> 1094  
 <212> PRT  
 <213> Drosophila melanogaster

<400> 35

Met Asn Ser Ala Val Asp Ala Trp Ala Val Thr Pro Arg Glu Arg Leu  
 1 5 10 15

Lys Tyr Gln Glu Gln Phe Arg Ala Leu Gln Pro Gln Ala Gly Phe Val  
 20 25 30

Thr Gly Ala Gln Ala Lys Gly Phe Phe Leu Gln Ser Gln Leu Pro Pro  
 35 40 45

Leu Ile Leu Gly Gln Ile Trp Ala Leu Ala Asp Thr Asp Ser Asp Gly  
 50 55 60

Lys Met Asn Ile Asn Glu Phe Ser Ile Ala Cys Lys Leu Ile Asn Leu  
 65 70 75 80

Lys Leu Arg Gly Met Asp Val Pro Lys Val Leu Pro Pro Ser Leu Leu  
 85 90 95

Ser Ser Leu Thr Gly Asp Val Pro Ser Met Thr Pro Arg Gly Ser Thr  
 100 105 110

Ser Ser Leu Ser Pro Leu Asp Pro Leu Lys Gly Ile Val Pro Ala Val  
 115 120 125

Ala Pro Val Val Pro Val Val Ala Pro Pro Val Ala Val Ala Thr Val  
 130 135 140

Ile Ser Pro Pro Gly Val Ser Val Pro Ser Gly Pro Thr Pro Pro Thr  
 145 150 155 160

Ser Asn Pro Pro Ser Arg His Thr Ser Ile Ser Glu Arg Ala Pro Ser  
 165 170 175

Ile Glu Ser Val Asn Gln Gly Glu Trp Ala Val Gln Ala Ala Gln Lys  
 180 185 190

Arg Lys Tyr Thr Gln Val Phe Asn Ala Asn Asp Arg Thr Arg Ser Gly  
 195 200 205

Tyr Leu Thr Gly Ser Gln Ala Arg Gly Val Leu Val Gln Ser Lys Leu  
 210 215 220

Pro Gln Val Thr Leu Ala Gln Ile Trp Thr Leu Ser Asp Ile Asp Gly  
 225 230 235 240

Asp Gly Arg Leu Asn Cys Asp Glu Phe Ile Leu Ala Met Phe Leu Cys  
 245 250 255



Glu Lys Ala Met Ala Gly Glu Lys Ile Pro Val Thr Leu Pro Gln Glu  
260 265 270

Trp Val Pro Pro Asn Leu Arg Lys Ile Lys Ser Arg Pro Gly Ser Val  
275 280 285

Ser Gly Val Val Ser Arg Pro Gly Ser Gln Pro Ala Ser Arg His Ala  
290 295 300

Ser Val Ser Ser Gln Ser Gly Val Gly Val Val Asp Ala Asp Pro Thr  
305 310 315 320

Ala Gly Leu Pro Gly Gln Thr Ser Phe Glu Asp Lys Arg Lys Glu Asn  
325 330 335

Tyr Val Lys Gly Gln Ala Glu Leu Asp Arg Arg Arg Lys Ile Met Glu  
340 345 350

Asp Gln Gln Arg Lys Glu Arg Glu Glu Arg Glu Arg Lys Glu Arg Glu  
355 360 365

Glu Ala Asp Lys Arg Glu Lys Ala Arg Leu Glu Ala Glu Arg Lys Gln  
370 375 380

Gln Glu Glu Leu Glu Arg Gln Leu Gln Arg Gln Arg Glu Ile Glu Met  
385 390 395 400

Glu Lys Glu Glu Gln Arg Lys Arg Glu Leu Glu Ala Lys Glu Ala Ala  
405 410 415

Arg Lys Glu Leu Glu Lys Gln Arg Gln Gln Glu Trp Glu Gln Ala Arg  
420 425 430

Ile Ala Glu Met Asn Ala Gln Lys Glu Arg Glu Gln Glu Arg Val Leu  
435 440 445

Lys Gln Lys Ala His Asn Thr Gln Leu Asn Val Glu Leu Ser Thr Leu  
450 455 460

Asn Glu Lys Ile Lys Glu Leu Ser Gln Arg Ile Cys Asp Thr Arg Ala  
465 470 475 480

Gly Val Thr Asn Val Lys Thr Val Ile Asp Gly Met Arg Thr Gln Arg  
 485 490 495

Asp Thr Ser Met Ser Glu Met Ser Gln Leu Lys Ala Arg Ile Lys Glu  
 500 505 510

Gln Asn Ala Lys Leu Leu Gln Leu Thr Gln Glu Arg Ala Lys Trp Glu  
 515 520 525

Ala Lys Ser Lys Ala Ser Gly Ala Ala Leu Gly Gly Glu Asn Ala Gln  
 530 535 540

Gln Glu Gln Leu Asn Ala Ala Phe Ala His Lys Gln Leu Ile Ile Asn  
 545 550 555 560

Gln Ile Lys Asp Lys Val Glu Asn Ile Ser Lys Glu Ile Glu Ser Lys  
 565 570 575

Lys Glu Asp Ile Asn Thr Asn Asp Val Gln Met Ser Glu Leu Lys Ala  
 580 585 590

Glu Leu Ser Ala Leu Ile Thr Lys Cys Glu Asp Leu Tyr Lys Glu Tyr  
 595 600 605

Asp Val Gln Arg Thr Ser Val Leu Glu Leu Lys Tyr Asn Arg Lys Asn  
 610 615 620

Glu Thr Ser Val Ser Ser Ala Trp Asp Thr Gly Ser Ser Ser Ala Trp  
 625 630 635 640

Glu Glu Thr Gly Thr Thr Val Thr Asp Pro Tyr Ala Val Ala Ser Asn  
 645 650 655

Asp Ile Ser Ala Leu Ala Ala Pro Ala Val Asp Leu Gly Gly Pro Ala  
 660 665 670

Pro Glu Gly Phe Val Lys Tyr Gln Ala Val Tyr Glu Phe Asn Ala Arg  
 675 680 685

Asn Ala Glu Glu Ile Thr Phe Val Pro Gly Asp Ile Ile Leu Val Pro  
 690 695 700

Leu Glu Gln Asn Ala Glu Pro Gly Trp Leu Ala Gly Glu Ile Asn Gly

705		710		715		720
His Thr Gly Trp Phe Pro Glu Ser Tyr Val Glu Lys Leu Glu Val Gly						
		725		730		735
Glu Val Ala Pro Val Ala Ala Val Glu Ala Pro Val Asp Ala Gln Val						
		740		745		750
Ala Asp Thr Tyr Asn Asp Asn Ile Asn Thr Ser Ser Ile Pro Ala Ala						
		755		760		765
Ser Ala Asp Leu Thr Ala Ala Glu Asp Val Glu Tyr Tyr Ile Ala Ala						
		770		775		780
Tyr Pro Tyr Glu Ser Ala Glu Glu Gly Asp Leu Ser Phe Ser Ala Gly						
		785		790		800
Glu Met Val Met Val Ile Lys Lys Glu Gly Glu Trp Trp Thr Gly Thr						
		805		810		815
Ile Gly Ser Arg Thr Gly Met Phe Pro Ser Asn Tyr Val Gln Lys Ala						
		820		825		830
Asp Val Gly Thr Ala Ser Thr Ala Ala Ala Glu Pro Val Glu Ser Leu						
		835		840		845
Asp Gln Glu Thr Thr Leu Asn Gly Asn Ala Ala Tyr Thr Ala Ala Pro						
		850		855		860
Val Glu Ala Gln Glu Gln Val Tyr Gln Pro Leu Pro Val Gln Glu Pro						
		865		870		875
Ser Glu Gln Pro Ile Ser Ser Pro Gly Val Gly Ala Glu Glu Ala His						
		885		890		895
Glu Asp Leu Asp Thr Glu Val Ser Gln Ile Asn Thr Gln Ser Lys Thr						
		900		905		910
Gln Ser Ser Glu Pro Ala Glu Ser Tyr Ser Arg Pro Met Ser Arg Thr						
		915		920		925
Ser Ser Met Thr Pro Gly Met Arg Ala Lys Arg Ser Glu Ile Ala Gln						
		930		935		940

Val Ile Ala Pro Tyr Glu Ala Thr Ser Thr Glu Gln Leu Ser Leu Thr  
 945 950 955 960

Arg Gly Gln Leu Ile Met Ile Arg Lys Lys Thr Asp Ser Gly Trp Trp  
 965 970 975

Glu Gly Glu Leu Gln Ala Lys Gly Arg Arg Arg Gln Ile Gly Trp Phe  
 980 985 990

Pro Ala Thr Tyr Val Lys Val Leu Gln Gly Gly Arg Asn Ser Gly Arg  
 995 1000 1005

Asn Thr Pro Val Ser Gly Ser Arg Ile Glu Met Thr Glu Gln Ile  
 1010 1015 1020

Leu Asp Lys Val Ile Ala Leu Tyr Pro Tyr Lys Ala Gln Asn Asp  
 1025 1030 1035

Asp Glu Leu Ser Phe Asp Lys Asp Asp Ile Ile Ser Val Leu Gly  
 1040 1045 1050

Arg Asp Glu Pro Glu Trp Trp Arg Gly Glu Leu Asn Gly Leu Ser  
 1055 1060 1065

Gly Leu Phe Pro Ser Asn Tyr Val Gly Pro Phe Val Thr Ser Gly  
 1070 1075 1080

Lys Pro Ala Lys Ala Asn Gly Thr Thr Lys Lys  
 1085 1090